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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
       Query
Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfIles1.pep:*
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US-09-378-238-11
US-09-378-238-12
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US-09-252-1498-34
US-09-252-1498-34
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US-09-252-1498-34
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                   VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375
                                                                              PICTURE STERROCKYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
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Query Match 100.0%; Score 630; DB 3; Ler Best Local Similarity 100.0%; Pred. No. 5.9e-66; Matches 109; Conservative 0; Mismatches 0; If	US-08-891-789B-2 US-08-891-789B-2 US-08-891-789B-2 Sequence 2, Application US/08891789B Sequence 2, Application US/08891789B Sequence 2, Application US/08891789B Sequence 2, Application US/08891789B FATELCANT: Grobet, Luc; Georges, Michel ITITLE OF INVENTION: Double-Muscling in Mammals NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSEE: Blake, Cassels & Graydon STREET: Box 25, Commerce Court West CITY: Toronto STATE: Ontario ZIP: M5L 1A9 COUNTRY: Canada COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage OPERATING SYSTEM: MS-DOS 5.1 SOFTWARE: WORD PERFECT COMPUTER: COWPAO, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1 SOFTWARE: WORD PERFECT CURRENT APPLICATION INFORMATION: APPLICATION NUMBER: US/08/891,789B FILING DATE: July 14, 1997 ATTORNEY/AGENT INFORMATION: NAME: Hunt, John C. REGISTRATION NUMBER: 52836/00004 FELECHMONICATION INFORMATION: TELEPHONE: (416) 863-4344 FELEFAX: (416) 863-4365 SEQUENCE CHARACTERISTICS: LENGTH: 375 amino acids TYPE: amino acid STRANDEDUSS: single TOPOLOGY: linear	ALIGNMENTS	28 618 98.1 376 4 US-09-252-149B-28 29 618 98.1 376 4 US-09-378-238-12 30 618 98.1 376 4 US-09-378-238-12 31 618 98.1 376 4 US-09-451-501-12 31 618 98.1 376 4 US-09-451-501-25 32 612 97.1 375 4 US-09-252-149B-30 33 608 96.5 375 4 US-09-252-149B-30 34 579 91.9 108 2 US-08-525-596B-8 36 579 91.9 108 4 US-09-378-238-8 37 579 91.9 108 4 US-09-378-238-8 38 573 5 91.0 126 1 US-09-451-501-8 39 573 5 91.0 126 1 US-08-247-907A-2 40 573 91.0 126 1 US-08-452-772-2 41 573 91.0 126 1 US-08-452-772-2 42 573 91.0 126 3 US-08-755-4 43 573 91.0 126 4 US-09-414-234-2 44 573 91.0 126 4 US-09-414-234-2 45 573 91.0 126 5 PCT-US94-05288-2
Length 375; Indels 0; Gaps 0;	u viene de la companya de la company		Sequence 28, Appl Sequence 12, Appl Sequence 12, Appl Sequence 25, Appl Sequence 30, Appl Sequence 33, Appl Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 24, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli

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US-08-525-596B-6
                         RESULT 4
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APPLICANT: Barker, Christopher A.
APPLICANT: MORSey, Mohamad
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
TITLE OF INVENTION: VERTEBRATE SUBJECTS
FILE REFERENCE: 9001-0042
CURRENT APPLICATION NUMBER: US/09/252,149B
CURRENT FILING DATE: 1999-02-18
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Best Local Similarity
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APPLICANT: Barker, Christopher A.

APPLICANT: Mozesy, Mohamad

TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN

TITLE OF INVENTION: VERTEBRATE SUBJECTS

FILE REFERENCE: 9001-0042

CURRENT APPLICATION NUMBER: US/09/252,149B

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: 60/075,213

PRIOR APPLICATION NUMBER: 60/075,213

PRIOR APPLICATION NUMBER: 60/075,213

PRIOR APPLICATION NUMBER: 690-02-19

NUMBER OF SEQ ID NOS: 39
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PRIOR FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
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TYPE: PRT
ORGANISM: bos taurus
-09-252-149B-2
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                                                                                       327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375
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100.0%; Pred. No. 5.9e-66;
ative 0; Mismatches 0;
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                                                                                                                                                                                                        Sequence 6, Application US/09177860A
Patent No. 6096506
GEMERAL INFORMATION:
APPLICANT: Huynh, Thanh
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GENERAL INFORMATION:
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SOPTWARE: PastSEQ for Wind
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/
FILING DATE: 19-SEP-1995
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D, J
REGISTRATION UNMBER: 31,678
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 678,678,679
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APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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MEDIUM TYPE: Diskett
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CITY: La Jolla
                                                                      CITY: San Diego
STATE: CA
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                                                 COUNTRY:
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amino acid
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                                                                                                       4365 Executive Drive, Suite 1600
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SYSTEM: Windows95
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                                                                                                                      Gray Cary Ware & Freidenrich LLP
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lee, Se-Jin

APPLICANT: Lee, Se-Jin

APPLICANT: Lee, Se-Jin

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC

TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN

TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES

PILE REFERENCE: JHU1120-9

CURRENT APPLICATION NUMBER: US/09/378,238

CURRENT APPLICATION NUMBER: 08/795,071

PARLIER APPLICATION NUMBER: 08/795,071

EARLIER PILING DATE: 1997-02-05

EARLIER FILING DATE: 1995-10-25

EARLIER APPLICATION NUMBER: 08/525,596

EARLIER FILING DATE: 1994-03-18

EARLIER FILING DATE: 1994-03-18

EARLIER APPLICATION NUMBER: 08/033,923

EARLIER FILING DATE: 1994-03-18

EARLIER FILING DATE: 1994-03-18

EARLIER FILING DATE: 1994-03-18

EARLIER FILING DATE: 1993-03-19

EARLIER FILING DATE: 1994-03-19
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                                                                                                                                                         ; ORGANISM: Mus musculus 
US-09-378-238-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-378-238-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09378238 Patent No. 6465239
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                                                                                                                                                                                                                                                           SEQ ID NO 6
                                                    Matches 107;
                                                                                                        Query Match
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NAME: Haile, Ph.D. Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 VHQANDRGSAGPCCTPTKMSPINMLYENGKEQIIYGKIPAMVVDRCGCS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VHQANDRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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                                                                              Similarity
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                                                      Conservative
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internal
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                                                                           98.1%;
98.2%;
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                                                 1; Mismatches
                                                                           Score 618; DB 4; Length 126; Pred. No. 4.2e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 618; DB 3; Length 126; Pred. No. 4.2e-65;
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                                                    1; Indels
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US-09-378-238-21
; Sequence 21, Application US/09378238
; Patent No. 6465239
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
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                                                                                                           RESULT 8
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PILING DATE: <UNKnown>
APPLICATION NUMBER: PCT/US94/03019

PILING DATE: 18-March-1994

ATTORNEY/AGENT INFORMATION:

NAME: Liea A. Haile, ph.D.

REGISTRATION NUMBER: 38,347

REGISTRATION NUMBER: 07265/105001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070

TELEPHONE: 619/678-5070

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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PATENT NO. 6468535
GENERAL INFORMATION:
APPLICANT: Se-Jin Lee et al.
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                       61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                         78 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 126
                                                                                                                                                                                                                                                                   18 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 77
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                                                                                                                                                                                                                                                                                               1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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OPERATING SYSTEM: Windows Ver:
SOFTWARE: FeateSEQ for Windows Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/451,501
FILING DATE: 30-NO. 6468535-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Se-Jin Lee et al.,
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                            98.1%; Score 618; DB 4; Length 126; 98.2%; Pred. No. 4.2e-65;
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US-09-378-238-19
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; ORGANISM: Rattus norvegicus
US-09-378-238-21
                                                                                                                                                                                                                     US-09-378-238-19
                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 08/033,923
EARLIER FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
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Best Local Similarity
                                                                                                       Matches
                                                                                                                                      Best
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Patent No. 646523
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
TITLE OF INVENTION: TRANSGERIC AQUATIC SPECIES
FILE REFERENCE: JHUI120-9
CURRENT FALING DATE: 1999-08-19
CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER APPLICATION NUMBER: 07/5596
EARLIER APPLICATION NUMBER: 07/5596
EARLIER FILING DATE: 1995-10-25
EARLIER FILING DATE: 1995-10-25
EARLIER FILING DATE: 1994-03-18
EARLIER FILING DATE: 1994-03-18
EARLIER FILING DATE: 1994-03-18
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EARLIER FILING DATE: 1997-02-05
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER APPLICATION NUMBER: PCT/US94/03019
EARLIER FILING DATE: 1994-03-18
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EARLIER FILING DATE: 1993-03-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, 1
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                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Gallus gallus
                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
117 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 176
                                                                                                       Local Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
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                              1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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                                                                                                                                      Similarity
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                                                                                                          Conservative
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98.2%; Pred. No. 4.3e-65;
tive 1; Mismatches 1; Indels
                                                                                                    98.1%; Score 618; DB 4; Length 225; 98.2%; Pred. No. 8.3e-65; tive 1; Mismatches 1; Indels
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Sequence 5, Application US/08765875
PAtent No. 5914234
GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: MCPHERRON, ALEXANDRA.
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                                                                                                                                                                                                                                                                                                                                                                                                 Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: Window SOFTWARE: Fast-SEQ for WI CURRENT APPLICATION DATA: APPLICATION NUMBER: US. APPLICATION DATE: 19-SEP-1995
                TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Wetherell, Jr., Ph.D, John R. REGISTRATION NUMBER: 31,678 REFERENCE/DOCKET NUMBER: 07285/0750 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400
  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                  1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                               VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
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SPENSLEY HORN JUBAS & LUBITZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              internal
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                                                                          ALEXANDRA C
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1880 CENTURY PARK EAST, FIFTH FLOOR

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Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                             Sequence 5, Application US/08795671
Patent No. 6008434
GENERAL INFORMATION:
GENERAL INFORMATION: GENERAL McPherron
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
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APPLICATION NUMBER: US/08/706,99

FILING DATE:

APPLICATION NUMBER: US/08/272,76

FILING DATE: 08-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: TUMARKIN PH.D., LISA A.

REGISTRATION NUMBER: P-38,347

REGISTRATION NUMBER: P-38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
ZIP: 9203/
COMPUTER READABLE FORM:
COMPUTER READABLE Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPETWARE: Patentin Release #1.0, Version #1.25
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/765,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE:
                                                                                                                                                                     ADDRESEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
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                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                         ADDRESSEE:
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1..375
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98.2%;
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Pred. No. 1.5e-64;
1; Mismatches 1;
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RESULT 13
US-09-177-860A-14
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APPLICATION: 424

FILING DATE: 23-OCT-1550

FILING DATA: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/525,596

FILING DATE: 19-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: Haile, Ph.D, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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Best Local Similarity 98.2
Matches 107; Conservative
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
                                                                                                                                                                                      SOFTWARE: FASCOCK
SOFTWARE: FASCOCK
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/
APPLICATION NUMBER: 23-OCT-1998
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NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/106001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                        STREET: ***
CTTY: San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
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ZIP: 92121
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1..375
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65 Executive Drive, Suite 1600
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                                                              07265/075003
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Pred. No. 1.5e-64;
1; Mismatches 1
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US-09-252-149B-29
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US-09-252-149B-32
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               GENERAL INFORMATION:
APPLICANT: Barker, Christopher A.
APPLICANT: Morsey, Mohamad
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
TITLE OF INVENTION: VERTERATE SUBJECTS
FILE REFERENCE: 9001-0042
CURRENT APPLICATION NUMBER: US/09/252,149B
CURRENT APPLICATION NUMBER: 1999-02-18
PRIOR APPLICATION NUMBER: 60/075,213
PRIOR FILING DATE: 1998-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/09252149B
Patent No. 6369201
GENERAL INFORMATION:
APPLICANT: Barker, Christopher A.
APPLICANT: Morsey, Mohamad
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
TITLE OF INVENTION: VERTEBRATE SUBJECTS
FILE REFERENCE: 9001-0042
CURRENT APPLICATION UNMBER: US/09/252,149B
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
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Best Local Similarity 98.2%;
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                     Sequence 32, Application US/09252149B Patent No. 6369201
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PRIOR FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 39
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SOFTWARE: FatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VHQANPRGSAGPCCTPTKMSPINMLYENGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                    327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 DFGLDCDEHSTESRCCRYPLTVDFBAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 98.1%;
Local Similarity 98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                    VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 618; DB 3;
Pred. No. 1.5e-64;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 618; DB 4; Length 375; Pred. No. 1.5e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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밁 Ś 밁 á US-09-252-149B-32 SEQ ID NO 32 LENGTH: 375 Matches Query Match Best Local Similarity TYPE: PRT ORGANISM: Sus scrofa 327 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375 267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326 61 VHQANPRGSAGECCTETKMSFINMLYFNGEGQIIYGKIPAMVVDRCGCS 109 1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECBFVFLQKYPHTHL 60 107; Conservative 98.1%; 98.2%; Score 618; DB 4; Length 375; Pred. No. 1.5e-64; Mismatches Indels Gaps

0

Search completed: January 31, 2003, 18:18:23 Job time : 11.5 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Geneseq 101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
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14: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
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28: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1000.DAT:*
29: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1000.DAT:*
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DFGLDCDEHSTESRCCRYPL.....EGQIIYGKIPAMVVDRCGCS 109
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqp~embl/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                             Length DB
      223320022
                                                                                                                                                                                                                                                                                                             IJ
                                  AAB20142
AAW69887
AAW33934
AAW331917
AAW311917
AAW31191
AAB20135
AAB20135
AAB18664
AAW97884
      AAB20141
                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                            Amino acid sequenc
Bovine myostatin s
Bovine GDF-8 prote
Cattle growth diff
                                                                                                                                                                                                                                                                                                       Description
Bovine promyostatin.
Bovine myostatin.
Human growth diffe
                                                                                                                                                                                                                      Cattle growth diff
Bovine growth diff
                                                                                       Bovine promyostati
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growth diff	AAB20131	22	375	98.1	618	Ų,
Human GDF-8 #2. H	AAB73187	22	375	98.1	618	-
growth diff	AAY77566	21	375	•	618	~
growth d	AAY92035	21	375		618	٠٠
GDF-8.	AAB21087	21	375	•	618	_
yostatin.	AAW97887	20	375	•	618	Ö
DF-8 I	AAY31194	20	375	•	618	w
-8 pro	AAY31192	20	375	•	618	w
œ	AAY31189	20	375		618	7
acid	AAY33935	20	375	98.1	618	٠,
	AAY33932	20	375	•	618	۷.
acid	AAY33938	20	375	•	618	-
	AAY33937	20	375	•	618	ω
	AAY33844	20	375		618	ı
	AAY33843	20	375		618	_
	AAY33841	20	375	98.1	618	_
acid	AAY33840	20	375	٠	618	w
acid	AAY33839	20	375	•	618	w
acid se	AAY33838	20	375	98.1	618	7
	AAW65460	19	375	•	618	U1
Human growth diffe	AAW69885	19	375		618	٠.
Pig growth differe	AAW69891	19	375	98.1	618	-
Chicken growth dif	AAW69888	19	375		618	<u></u>
Human growth diffe	AAR63160	15	375	98.1	618	١٠
Chicken promyostat	AAU75623	23	374	•	618	_
Turkey growth diff	AAB20132	22	362	•	618	_
different	AAB20152	22	254	٠	618	w
1 GDF-8. G	AAB73188	22	226		618	w
wth differenti	AAB20153	22	160	•	618	7
-8. Rat	AAB73189	22	130	•	618	٠,
1	AAB73182	22	126	•	618	0,
nal region	AAY15386	20	126	•	618	-
e growti	AAW69883	19	126	•	618	~
growth diff	AAR63161	15	126	98.1	618	
Human TGFbeta prot	AAM51935	23	109	•	618	_

## ALIGNMENTS

RESULT 1 AAB20142

Cattle growth differentiation factor 8 C-terminal region.

30-APR-2001 (first entry)

AAB20142;

AAB20142 standard; Protein; 109 AA.

```
Increasing the muscle mass of animals used in meat production by down regulating growth differentiation factor 8 (GDF-8) activity in the
                                WPI; 2001-112680/12.
                                                                                          20-JUL-1999;
26-JUL-1999;
                                                                                                                        20-JUL-2000; 2000WO-DK00413
                                                                                                                                                                                   Bos taurus.
Synthetic.
                                                                                                                                                                                                                 Growth differentiation factor 8; GDP-8; myostatin; down-regulation; vaccine; muscle; meat; cachexia; cardiant; cattle; mutant; mutein.
                                                  Halkier T, Mouritsen S,
                                                                                                                                            25-JAN-2001.
                                                                                                                                                                WO200105820-A2.
                                                                       (MEBI-) M & E BIOTECH AS
                                                                                          99DK-0001014
99US-0145275
                                                   Klysner S;
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animal through induction of anti-GDF-8 antibody production

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RESULT 2
AAM6
XX
ACC AAM6
XX
OPEN
ACC AAM6
AC
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are provided that are capable of breaking autocolerance against
cautologous GDF-8. These comprise the C-terminal portion of human
GDF-8 in which a portion of the native sequence is replaced by a
T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
T-cell epitop
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         23-MAY-1997;
05-FEB-1937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Growth differentiation factor-8; GDF-8; human; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence comprises the 109 amino acid residue C-terminal region of cattle growth differentiation factor 8 (GDF-8). i.e. residues 267-375 of the full-length protein (see AAB20132). The homodimer of this region is thought to be the biologically active form of GDF-8. It is an object of the invention to produce a recombinant therapeutic vaccine capable of effecting down-regulation of GDF-8 in order to increase the muscle growth rate of farm animals. Variants of GDF-8 (see AAB20145-53)
                                                                                                                                                                                                                       06-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW69887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                              05-FEB-1998;
                                                                                                                                                                                                                                                                                                       W09833887-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine growth differentiation factor-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW69887 standard; Protein; 375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 94-95; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VHQANPRGŠAGPCCTPTKMSPINMLYFNGBGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
    97US-0862445
97US-0795071
                                                                                                                         98WO-US02479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 630; DB 22;
100.0%; Pred. No. 1.8e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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Bos sp.

mammary gland tissue; lactation; feed uptake; muscle degeneration; GDF11

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC and adipose tissue. The sequence was deduced from a cDNA clone CC (see AAV45818) isolated from a skeletal muscle cDNA clone CC invention provides novel mammalian and avian GDP-8 proteins (see CC AAW5983-92). A transgenic non-human animal is claimed in which CC GDP-8 expression is disrupted or interfered with. Also claimed CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb CC animals by administering an antibody (Ab) that binds to GDF-8; (3) CC inhibiting the action of GDP-8 by treating foetal or abilt muscle CC arid encoding a GDP-8 protein truncated by loss of the C-terminal CC active fragment. The transgenic animals have increased muscle mass CC and for poultry reduced cholesterol contents. Method (3) is used to treat muscle wested poultry reduced cholesterol contents. Method (3) is used to treat muscle injuries, congestive or obstructive lung disease, AIDS CC and aging, particularly muscular dystrophy, spinal cord or traumatic injuries, congestive or obstructive lung disease, AIDS CC and cachexia. Method (4) is used to treat cancer of muscle CC and cachexia. Method (4) is used to treat cancer of muscle CC and seed to maintain myblasts intended for transplanting or to CC improve efficiency of fusion. Ab can be used to detect and CC quantify GDP-8 (particularly in muscle, for diagnosis or monitoring), cross also for immunotherapy and in vivo imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                09-NOV-1999 (first entry)
                                                                                                                                                                 AAY33934;
Myostatin; mouse; rabbit; human; baboon; bovine; porcine; ovine; chick; turkey; zebrafish; immune response; vaccine; body weight; muscle mass;
                                                                       Amino acid sequence of bovine myostatin.
                                                                                                                                                                                                             AAY33934 standard; peptide; 375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of bovine growth differentiation factor-8 (GDF-8), a novel member of the transforming growth factor-beta superfamily that appears to relate to various cell proliferative disorders, especially those involving muscle, nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contents, also use of GDF-8 inhibitors for treating cancer, obesity, neuromuscular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 9; Fig 14b; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                             327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                     267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                               61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1998-437444/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McPherron AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV45818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0847910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 630; DB 19;
Pred. No. 6.7e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 375;
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RESULT 4
AAY33/T ID AAY3
XX AAY3
XX AAY3
XX BOVI
XX BOVI
XX BOVI
XX BOVI
XX MYOS
XX MYOS
XX MYOS
XX MADET
XX GDEPT
XX GDEPT
FT Clea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides myostatin peptides consisting of 3-100 amino acids, derived from a region of mouse, rabbit, human, baboon, bovine, porcine, ovine, chick, turkey or zebrafish myostatin (see sequences AAY33930-939). The myostatin peptides are derived preferably from a region of amino acid residues 1-275, 25-300, 50-325 or 75-350 of the above sequences. The peptides and the nucleic acids encoding the peptides are useful as vaccines for eliciting an immune response in a vertebrate against a myostatin immunogen. They result in increasing body weight, muscle mass, number and size of muscle cells, muscle strength, mammary gland tissue, lactation, appetite or feed uptake, life span of the vertebrate, and cause a reduction in body fat content, useful for muscle wasting conditions. The vaccines are also useful for treating a disorder which comprises degeneration or wasting of muscle in a vertebrate, and useful for modulating GDPII activity. The present sequence represents
                                                                                                                                                                                                                                                                                     09-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Fig 1A-D; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New myostatin peptide, multimers and immunoconjugates for eliciting an immune response in a vertebrate against a myostatin immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barker CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-1999
                                                                                                                                                                  Myostatin; mouse; rabbit; human; baboon; bovine; porcine; ovine; chick; turkey; zebrafish; immune response; vaccine; body weight; muscle mass; mammary gland tissue; lactation; feed uptake; muscle degeneration;
                                                                                                                                                                                                                                              Bovine myostatin sequence.
                                                                                                                                                                                                                                                                                                                        AAY33917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOS-) BIOSTAR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9942573-A1
                                                                                                              ds sog
                                                                                                                                                   GDF11 activity
                                                                                                                                                                                                                                                                                                                                                               AAY33917 standard; Protein; 375 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          327
                                                        Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bovine myostatin segeunce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                          VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morsey M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0075213.
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                                                      Location/Qualifiers 263..266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                     .375
"myostatin active region"
                                  "proteolytic cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 630; DB 20;
Pred. No. 6.7e-59;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                            RESULT 5
AAY31191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides myostatin peptides consisting of 3-100 amino caids, derived from a region of mouse, rabbit, human, baboon, bovine, porcine, ovine, chick, turkey or zebrafish myostatin (see sequences C porcine, ovine, chick, turkey or zebrafish myostatin (see sequences C ANY3330-939). The myostatin peptides are derived preferably from a region of amino acid residues 1-275, 25-300, 50-325 or 75-350 of the cabove sequences. The peptides and the nucleic acids encoding the peptides are useful as vaccines for eliciting an immune response in a vertebrate cagainst a myostatin immunogen. They result in increasing body weight, muscle mass, number and size of muscle cells, muscle strength, mammary gland tissue, lactation, appetite or feed uptake, life span of the comprises degeneration or wasting of muscle useful for muscle wasting conditions. The vaccines are also useful for treating a disorder which comprises degeneration or wasting of muscle in a vertebrate, and cuse of special for modulating dDF11 activity. The present sequence represents the amino acid sequence of bovine myostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                    GDF-8; growth differentiation factor receptor; GDF-11; therapy; human; veterinary; medicine; treatment; muscle tissue disease; wasting disease; neuromuscular disorder; muscular atrophy; spinal cord injury; aging; fat; traumatic injury; acquired immune deficiency syndrome; cachexia; bovine; congenital obstructive pulmonary disease; transgenic animal; transgene; food animal; cholesterol; muscle mass; diagnostic.
                                                                                                                                                                                                                                                                                                                                           AAY31191 standard; Protein; 375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New myostatin peptide, multimers and immunoconjugates for eliciting an immune response in a vertebrate against a myostatin immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX99349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barker CA, Morsey M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-AUG-1999.
                                                                                                                                                                                                                          Bovine GDF-8 protein.
                                                                                                                                                                                                                                                                                                        AAY31191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 16B; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-527471/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIOS-) BIOSTAR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9942573-A1
                   WO9906559-A1.
                                                        Bos taurus.
                                                                                                                                                                                                                                                                      29-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                        327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9805-0075213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-CA00128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 630; DB 20; 100.0%; Pred. No. 6.7e-59; tive 0; Mismatches 0;
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Indels Length 375;

0;

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel recombinant cell lines that express CC growth-differentiation factor-8 (GDF-8) receptor polypeptide or GDF-11 CC (earl) approises. The GDF receptors are used to identify specific CC (ant) agonists, potentially useful therapeutically in human or veterinary CC medicine. Antibodies derived from the products of the invention are used to treat muscle tissue diseases (particularly wasting diseases, communicated and somatic cells, specifically where GDF-8 receptor is expressed, compensed muscle mass. Peptides derived from the products of the invention and GDF-receptor binding and blocking agents, are reagents and convention and GDF-receptor binding and blocking agents, are reagents and compension of the speculic agents. This sequence represents the bovine CC GDF-8 protein which is used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
20-JUL-20@0; 2000WO-DK00413.
                                                                                                                                         Growth differentiation factor 8; GDF-8; myostatin; down-regulation; vaccine; muscle; meat; cachexia; cardiant; cattle.
                                                                                                                                                                                                Cattle growth differentiation factor
                                                                                                                                                                                                                                  30-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant cells that express growth-differentiation factor receptors - and related antibodies, nucleic acids, vector, transformed cells, peptide fragments and transgenic animals, for treatment and diagnosis of muscle tissue diseases
                                      25-JAN-2001.
                                                                        WO200105820-A2
                                                                                                           Bos taurus.
                                                                                                                                                                                                                                                                       AAB20135;
                                                                                                                                                                                                                                                                                                     AAB20135 standard; Protein; 375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Examples; Fig 2b; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                              327
                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                        1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-153789/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ09367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 630; DB 20;
Pred. No. 6.7e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of cattle growth differentiation factor (8 (GDF-8), also called myostatin. It is an object of the invention to produce a recombinant therapeutic vaccine capable of effecting down-regulation of GDF-8 in order to increase the muscle growth rate of farm animals. Variants of GDF-8 (GDF-8 (GDF-8)) are provided that are capable of breaking autocolerance against autologous GDF-8. These comprise a C-terminal portion of human GDF-8 in which a portion of the native sequence is replaced by a recombination of the native sequence is replaced by a recombination of the native sequence is call epitope such as the promiscuous tetanus toxin T-call spitope and a series encoding the GDF-8 variants can be used for genetic immunisation of the animals. Down-regulation of GDF-8 activity is used to increase muscle mass by up to at least 45% in cattle, pigs and poultry used for meat production, reducing the need for antibiotic feed-additives. Anti-GDF9 vaccines can be used to treat human diseases such as cancer cachexia where muscle atrophy heart failure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                            Bovine; promyostatin; myostatin; therapy; amyotrophic lateral sclerosis; neurodegenerative disease; GDF-11; muscular dystrophy; type II diabetes; muscle growth; myostatin prodomain; signal transduction; atherosclerosis; obesity; cachexia; hypertension; myocardial infarction; neuroprotective; muscular dystrophy; muscle wasting disorder; neuromuscular disorder; anorexia; growth differentiation factor; anorectic; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                            Domain
                                                                                                      Bos sp
                                                                                                                                                cardiant;
                                                                                                                                                                                                                                                                                                             Bovine promyostatin.
                                                                                                                                                                                                                                                                                                                                                       17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                               AAE18664;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE18664 standard; Protein; 375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 82-83; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Increasing the muscle mass of animals used in meat production by down regulating growth differentiation factor 8 (GDF-8) activity in the animal through induction of anti-GDF-8 antibody production -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-112680/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEBI-) M & E BIOTECH AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                   (first entry)
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99US-0145275.
/note= "Myostatin prodomain; This region is specifically
claimed in claim 12 of the specification"
                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 630; DB 22; 100.0%; Pred. No. 6.7e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klysner S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 375;
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The present invention relates to a purified promyostatin polypeptide CC portion. A myostatin peptide is useful as a target for treatment of CC neurodegenerative diseases such as amyotrophic lateral sclerosis or CC transduction, while mature myostatin prodomain inhibits myostatin signal CC transduction, while mature myostatin peptide referred as myostatin is CC useful for inducing myostatin signal transduction by interacting CC specifically with myostatin receptor expressed on the surface of the CC cell. Modulating myostatin signal transduction is useful for regulating CC skeletal muscle mass, where promyostatin portion is a negative regulator CC rausele growth Modulating myostatin signal transduction in a muscle CC cell or adipose tissue is useful for treating pathological conditions associated with myostatin such as obesity and type II diabetes, cachexia, CC myocardial infarction, muscle wasting disorders such as muscular CC dystrophy, neuromuscular disorders, or anorexia. Myostatin prodomain is useful for modulating the growth of muscle mass or CC organism. Myostatin prodomain is useful for increasing muscle mass or CC complete content of an organism which is useful as a food source, and myostatin peptide is useful for decreasing the growth of muscle mass or CC myostatin which has dominant negative activity with respect to myostatin or growth differentiation factor (CDP)-II is useful for reducing or inhibiting myostatin farential transduction. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel substantially purified promyostatin polypeptide portion (myostatin prodomain or mature myostatin peptide), useful as myostatin signal transduction modulator in muscle cell or adipose tissue, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200209641-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUL-2000; 2000US-0628112
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    21-MAY-2002
                                                                             AAU75625;
                                                                                                                                                     AAU75625 standard; Protein; 375 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence is bovine promyostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating obesity
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                                                                                                                                                                                                                                                                                                                                              327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                      61 VHOANPRGSAGECCTETKMSPINMLYFNGEGOIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibiting myostatin signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
(first entry)
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claimed in claim 17 of the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Pred. No. 6.7e-59;
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Myostatin; cattle; bovine; transforming growth factor beta; double muscling; muscle hyperplasia; transgenic animal.

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a substantially purified growth differentiation factor (GDF) receptor, specifically a myostatin receptor, or its functional peptide portion. Also described is a method of modulating an effect of myostatin on a cell by contacting the cell with an agent that affects myostatin signal transduction in the cell. The method and the receptor are useful for ameliorating the severity of a pathological condition characterised by an abnormal amount, development or metabolic activity of muscle or adipose tissue in a subject, particularly a wasting disorder (e.g. cachexia, anorexia, muscular dystrophy or neuromuscular disease) or a metabolic disorder (e.g. obesity or type II diabetes). The present sequence represents the amino acid sequence of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New growth differentiation factor (GDF) receptors and modulators, useful for ameliorating wasting disorders such as cachexia, muscular dystrophy or neuromuscular disease or a metabolic disorder such as obesity or type II diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2001; 2001WO-US23615
                                                                                                          AAW97884;
                                                                                                                                        AAW97884 standard; Protein; 375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Fig 1; 184pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JUL-2000; 2000US-0626896
                                            Bovine myostatin.
                                                                            07-JUN-1999
                                                                                                                                                                                                                      327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                           61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                  2002-217116/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                  375 AA;
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                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                  Score 630; DB 23;
Pred. No. 6.7e-59;
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RESULT 10
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AC AAB20
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DT 30-AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CC This is the amino acid sequence of bovine myostatin, a member of CC the transforming growth factor beta superfamily, as encoded by the CC wild-type gene (see AAX24416). A mutation of this gene (see AAX24416) CC has been detected in cattle. Cattle of the Beigian Blue breed CC homozygous for the mutant gene are double-muscled. A new method of CC increasing muscle mass of a mammal having myostatin-expressing cC muscle cells, complementary to at least a portion of mRNA cencoding myostatin and of sufficient length to reduce myostatin expression and thus increase muscle mass. A ribozyme may also be CC used. Also claimed are: a method for determining muscular C hyperplasia (MH) in a mammal susing primers based upstream and constream of the mutation; a diagnostic kit for determining CC determining MH in a mammal; a method for determining the myostatin cC genotype of a sample of genetic material; a method for determining the myostatin cC muscling in a bovine animal; a method for determining the myostatin cC muscling host cell; a probe based on the myostatin gene cutive myostatin, and a heterologous nucleotide sequence encoding a crive myostatin, and a heterologous nucleotide sequence antisense cc to that gene, and optionally further containing a gene encoding a cutive myostatin, and a heterologous nucleotide sequence antisense cc to that gene, and optionally further containing a gene encoding a colleic acid sequence with ribozyme activity in transcriptional axis association with the antisense sequence.
                                                                                                                                                                                                                                                                                                                                                          Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Human growth differentiation factor 8 C-terminal region
                                       30-APR-2001
                                                                                                               AAB20141 standard; Protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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14-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 19; Page 55; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Increasing muscle mass in mammals - by decreasing myostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX24415, AAX24464.
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                                                                                                                                                                                                                              61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  375 AA;
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                                   (first entry)
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97US-0891789
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                                                                                                                                                                                                                                                                                                                                                      Score 624; DB 20;
Pred. No. 2.9e-58;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                        1; Indels
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61

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61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109

VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109

1 DFGLDCDEHSTESRCCRYPLIVDFBAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60

0

DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60

AAM51935

AAM51935 standard; protein; 109 AA

AAM51935;

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X88X88X
                                                                                                                                                                                                                                                     The present sequence comprises the 109 amino acid residue CC C-terminal region of human growth differentiation factor 8 (SC CDF-8), i.e. residues 267-375 of the full-length protezin (see CC ABB20131). The homodimer of this region is thought to be the biologically active form of GDF-8. It is an object of the biologically active form of GDF-8 in tis an object of the muscle CC invention to produce a recombinant therapeutic vaccine capable of CC effecting down-regulation of GDF-8 in order to increase the muscle CC growth rate of farm animals. Variants of GDF-8 (see ABB20145-53) CC are provided that are capable of breaking aurotolerance against autologous GDF-8. These comprise the C-terminal portion of human CC GDF-8 in which a portion of the native sequence is replaced by a CC reell epitope such as the promiscuous tetanus toxin T-cell epitope CP 2 or P30. The high number (9) of Cys residues in the C-terminal CC positioned without major disturbance of the native 3-dimensional CC structure of the protein. Nucleic acids encoding the GDF-8 variants CC can be used for genetic immunisation of the animals. Down-regulation CC GADF-8 activity can increase muscle mass by up to at least 45% in CC cattle, pigs and poultry used for meat production, reducing the need CC treat human diseases such as cancer cachasia where muscle atrophy is corronanced and for patients suffering from acute and chronic heart
                                     Query Match
Best Local
           Matches
                                                                                                                                     Seguence
                                                                                                                                                                                                                                         pronounced and for patients suffering from acute and chronic heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 93-94; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Increasing the muscle mass of animals used in meat production by down regulating growth differentiation factor 8 (GDP-8) activity in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1999;
26-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               animal through induction of anti-GDF-8 antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-112680/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-2000; 2000WO-DK00413.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MEBI-) M & E BIOTECH AS
       107;
                                        Similarity
                                                                                                                                         109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouritsen S,
       Conservative
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99US-0145275
                                 98.1%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klysner S;
   1; Mismatches
                                     Score 618; DB 22;
Pred. No. 3.4e-58;
                                                                      DB 22; Length 109;
       Indels
       0,
Gaps
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RESULT 12
AAR63161
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to muteins of a chain of a protein which, when in the form of a homodimer, has antagonistic or partial agonistic activity, and where the mutation results in the protein binding with low affinity to its receptor. The protein is a member of the transforming growth factor beta (TGFbeta) superfamily. The mutant sequences of the invention can be used in the treatment of diseases associated with the overexpression of TGFbeta family proteins, including ectopic bone formation, psoriasis, muscular atrophy, scar formation, fibrosis and cirrhosis. The present sequence is the human GDF8 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; TGFbeta; transforming growth factor beta; mutant; antagonist; agonist; ectopic bone formation; psoriasis; muscular atrophy; scar; formation; fibrosis; cirrhosis; osteopathic; antipsoriatic; antifibrotic; hepatotropic; vulnerary; GDF8.
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mutein of transforming growth factor-beta superfamily protein, useful for treating or preventing e.g. ectopic bone formation, competes for receptor binding -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sebald W, Nickel J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000; 2000DE-1026713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE10026713-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                    Growth differentiation factor-8; GDF-8; cell proliferation; adipocyte; obesity; transforming growth factor-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 6; 54pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-042559/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000; 2000DE-1026713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TGFbeta protein superfamily protein GDF8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2002 (first entry)
           W09421681-A.
                                                                                       Mouse growth differentiation factor-8 partial sequence.
                                                                                                                                                        AAR63161 standard; Protein; 126 AA.
                                 Mus musculus.
                                                                                                             23-JUN-1995 (first entry)
                                                                                                                                  AAR63161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SEBA/) SEBALD W.
                                                                                                                                                                                                                                    61
                                                                                                                                                                                                              61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                        1 DFGLDCDEHSTESRCCRYPLITVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                          1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                            VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                       107;
                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                  109 AA;
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                                                                                                                                                                                                                                                                                                             98.1%;
98.2%;
                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                              Score 618; DB 23;
Pred. No. 3.4e-58;
                                                                                                                                                                                                                                                                                                                         Length 109;
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ID AAW69
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Best Local s
                                                                                                                                                                                                                        Mus sp.
                                                                                                                                                                                                                                                                                                                                                  AAW69883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-1994.
Lee S,
                                                       23-MAY-1997;
05-FEB-1997;
                                                                                                                                                                                                                                              therapy
                                                                                       05-FEB-1998;
                                                                                                             06-AUG-1998
                                                                                                                                                                    Protein
                     (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                           28-APR-1997;
                                                                                                                                  WO9833887-A1
                                                                                                                                                                              Cleavage-site
                                                                                                                                                                                          Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                               78
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)B; Q76380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcpherron AC;
McPherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 AA;
                                          97US-0862445.
97US-0795071.
97US-0847910.
                                                                                       98WO-US02479.
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GDF-8 can be used to maintain cells before transplantation; to improve efficiency of cell fusion and to treat obesity or diseases related to abnormal adipocyte proliferation.
                                                                                                                                                                                                                                             Growth differentiation factor-8; GDF-8; mouse; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
                                                                                                                                                                                                                                                                                                                                                              Murine growth differentiation factor-8 C-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 41; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New growth differentiation factor 8 - useful for treatment and diagnosis of cell proliferative disorders esp. of muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW69883 standard; Protein; 126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0033923.
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                            16..17
17..126
                                                                                                        Location/Qualifiers
/note= "mature polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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Pred. No. 4e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COPT-8 expression is disrupted or interfered with. Also claimed are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb if from these animals; (2) method for increasing muscle mass in animals by administering an antibody (Ab) that binds to GDP-8; (3) in hibiting the action of GDP-8 by treating foetal or adult muscle or progenitor cells with a GDP-8 inhibitor; (4) isolated mucleic or progenitor cells with a GDP-8 inhibitor; (4) isolated mucleic active fragment. The transgenic animals have increased muscle mass and agring, particularly muscular diseases, muscular atrophy traumatic injuries, congestive or obstructive lung disease, AIDS and againg, particularly muscular dystrophy, spinal cord or craumatic injuries, congestive or obstructive lung disease, AIDS and cachexia. Method (4) is used to treat cancer of muscle, for can be used to maintain myoblasts intended for transplanting or to improve efficiency of fusion. Ab can be used to detect and quantify GDP-8 (particularly in muscle, for diagnosis or monitoring), also for improverse for improverse for fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth differentiation factor-b (GULT-U), controlled the transforming growth factor-beta superfamily those involving to various cell proliferative disorders, especially those involving muscle, nerve and adipose tissue. The sequence was deduced from a partial genomic clone (see ANV45809). A full-length sequence (see ANV45809) has been deduced from a cDNA clone (see ANV2113). The invention provides novel meammalian and avian GDF-8 proteins (see ANW65883-92). A transgenic non-human animal is claimed in which ANW65883-92). A transgenic non-human animal is claimed in which
                                                                                                                         growth differentiation factor; tissue growth; muscle growth; cell differentiation; animal feed; muscle disorder; bone degeneration; nerve degeneration; GDF-8; development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol content also use of GDP-8 inhibitors for treating cancer, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of the C-terminal portion of mouse growth differentiation factor-8 (GDF-8), a novel member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-437444/37.
N-PSDB; AAV45809.
  Cleavage-site
                                                                   Mus musculus
                                                                                                          transforming growth factor beta; TGF-beta.
                                                                                                                                                                                                                   C-terminal region of mouse Growth Differentiation Factor-8 (GDF-8).
                                                                                                                                                                                                                                                                  08-DEC-1999
                                                                                                                                                                                                                                                                                                                                                 AAY15386 standard; Protein; 126 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      also for immunotherapy and in vivo imaging.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuromuscular disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              госат
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 AA;
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                                                                                                                                                                                                                                                               (first entry)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of the C-terminal region of the GDP-8 precursor protein. The predicted GDF-8 sequence contains two potential proteolytic processing sites.

Cleavage of the precursor at the second of these sites would generate a mature C terminal fragment 109 amino acids in length with a predicted molecular weight of 12,400.

GDF-8 has been shown to result in increased bone and muscle mass (such as ribs) when expressed in reduced amounts. GDF-8 minus transgenic animals and forms of animal feed that can inhibit/reduce production of GDF-8 are of commercial interest.
Gene therapy; growth differentiation factor-8; OBF-8; AIDS; cachexia; neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculodegenerative disease; tissue repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDF-8 expression may also have a role in the therapy of abnormal growth of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8 antisense molecule or dominant negative polypeptide could be used with foetal or adult muscle cells, bone cells or progenitor cells. These agents can be administered to a patient suffering from a disorder such as muscle wasting disease, neuro muscular disorder, muscle atrophy, osteoporosis, bone degenerative diseases, obesity or other adiporte
                                                                         Murine GDF-8 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                           11-MAY-2001
                                                                                                                                                AAB73182;
                                                                                                                                                                                AAB73182 standard; Protein; 126 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ06446.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9940181-A1
                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                        61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                             1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders, and aging for example.
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16...17
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/note= "cleavage generates mature protein"
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Pred. No. 4e-58;
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Search completed: January 31, 2003, 18:20:11 Job time : 33 secs
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Matches 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to growth differentiation factor-8 (GDF-8) coding sequences and proteins. The present sequence is a GDF-8 protein, which was isolated in the present invention. GDF-8 is useful for treating neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular dystrophy), musculodegenerative diseases or in tissue repair due to trauma, obesity and disorders related to abnormal proliferation of adipocytes. GDF-8 is also useful for treating malignancies of the various organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, spinal cord injury, traumatic injury, congestive obstructive pulmonary disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New substantially purified growth differentiation factor-8 polypeptide, useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome and cachexia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                muscle wasting disease; neuromuscular disorder; spinal cord injury; traumatic injury; congestive obstructive pulmonary disease.
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N-PSDB; AAF63547.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COPD), AIDS or cachexia.
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nes 107; Conserv
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ilarity 98.2%;
Conservative
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Pred. No. 4e-58;
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Perfect score:
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
   US-09-841-730-12
US-09-859-211-21
US-09-859-211-3
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Sequence 12, Appl
Sequence 21, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 35, Appli
Sequence 8, Appli
Sequence 14, Appl
Sequence 14, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 29, Appl
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Sequence 5, Appl
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Sequence 12, Appl
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	ū	1-730-12 I. Applics No. US2002011 L INFORMATION CANT: Lee, Se OF INVENTION REFERENCE: JH NT APPLICATION NT FILING DATE: APPLICATION APPLICATION FILING DATE: APPLICATION NFILING DATE: APPLICATION FILING DATE: APPL		618 612 612 611 611 608 608 573 573 573 573 573 573 573 573 573 573
VHQANPRGSAGPCCTPTKMS              VHQANPRGSAGPCCTPTKMS	al similarity 109; Conserva DFGLDCDEHSTESRC	ENGILT 1  S-03-641-730-12  Sequence 12, Application US/09841730  Batent No. US20020157126A1  GENERAL INFORMATION:  APPLICANT: Lee, Se-Jin  APPLICANTON: GROWTH DIFFEREN  TITLE OF INVENTION: GROWTH DIFFEREN  TITLE OF INVENTION: GROWTH DIFFEREN  CURRENT EPLICATION NUMBER: US/09/8  CURRENT FILING DATE: 2000-07-27  PRIOR APPLICATION NUMBER: PCT/US98/ PRIOR APPLICATION NUMBER: PCT/US98/ PRIOR APPLICATION NUMBER: G0/054,46  PRIOR APPLICATION NUMBER: G0/054,46  PRIOR FILING DATE: 1998-07-28  PRIOR APPLICATION NUMBER: G0/054,46  PRIOR FILING DATE: 1997-08-04  NUMBER OF SEQ ID NOS: 29  SOFTWARE: FASTSEQ for Windows Verei  SEQ ID NO 12  LENGTH: 375  TYPE: PRT  ORGANISM: Bovine  15-09-841-730-12		998 997 997 997 997 997 997 997
CTPTKMS		Jin Alexan GROWTH DI ACOUSTS 11470-2 IN TUMBER: U UNMBER: 07-27 UNMBER: ECT 1998-07-28 S: 200-01-31 Ji 998-07-28 GOT Windows Cor Windows C		375 375 375 375 375 375 375 375 4407 108 4407 1128 4407 1128 4407 1128 4407 1128 4407 1128 4407 1128 4407 1128 1128 1128 1128 1129 1129 1129 1129
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PINMLYPNGEGQIYGKIPAMVVDRCGCS 	Pred. No. 7.2e-59; 0; Mismatches 0; PEAFGWDWIIAPKRYKANYCS	TIATION FACTOR RECEP NTACONISTS THEREOF, 41,730 6 6 6 15598	ALIGNMENTS	US-09-859-894A-11 US-09-859-211-13 US-09-859-211-19 US-09-859-211-19 US-09-859-211-11 US-09-859-211-11 US-09-859-211-11 US-09-859-211-11 US-09-859-894A-4 US-09-859-894A-2 US-09-859-894A-2 US-09-859-894A-2 US-09-859-894A-2 US-09-811-30-29 US-09-811-30-29 US-09-811-30-29 US-09-811-30-29 US-09-811-30-29 US-09-811-30-29 US-09-811-30-29 US-09-813-398-20 US-09-859-211-46 US-09-859-211-46 US-09-859-211-46 US-09-859-211-46 US-09-859-211-46 US-09-859-211-398-20 US-09-813-398-20 US-09-813-398-22 US-09-813-398-22 US-09-813-398-22 US-09-813-398-22 US-09-813-398-22 US-09-813-398-22
s 109     375	12-C	AND METHODS OF USING SAME		Sequence 11, Appl Sequence 5, Appli Sequence 10, Appl Sequence 19, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 21, Appli Sequence 25, Appli Sequence 25, Appli Sequence 27, Appli Sequence 20, Appli Sequence 20, Appli Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 20, Appl Sequence 21, Appl Sequence 20, Appl

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US-09-859-211-6
Sequence 6, Application US/09859211
Patent No. US20020157125A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 08/662,445
PRIOR FILING DATE: 1997-05-23
PRIOR PEPLICATION NUMBER: 08/847,910
PRIOR PEPLICATION NUMBER: 08/847,910
PRIOR PEPLICATION NUMBER: 08/795,071
PRIOR PEPLICATION NUMBER: 08/525,596
PRIOR APPLICATION NUMBER: 08/525,596
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SOFTWARE: FAST:
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FRACTH: 375
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TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: U8/09/859,211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR FILING DATE: 1998-02-05
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PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
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PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR PLICATION NUMBER: 08/95,071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
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PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
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CURRENT FILING DATE: 2001-05-15
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APPLICANT: McPhetron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
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APPLICANT: MCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Se-Jin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07265/144001
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PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILLING DATE: 1997-02-05
PRIOR PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILLING DATE: 1995-10-26
PRIOR FILLING DATE: 1994-03-18
PRIOR FILLING DATE: 1994-03-18
PRIOR FILLING DATE: 1994-03-18
PRIOR FILLING DATE: 1994-03-18
PRIOR FILLING DATE: 1993-03-19
PRIOR FILLING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SOFTMARE: FASTESEQ FOR WINDOWS Version 4.0
SEQ ID NO 33
PRIOR FILLING DATE: 1995-03-19
NUMBER OF SEQ ID NOS: 51
SEQ ID NO 33
PRIOR FILLING DATE: 1995-03-19
NUMBER OF SEQ ID NOS: 51
PRIOR DATE: 130
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APPLICANT: McCherron, Alexandra C.
APPLICANT: McCherron, Alexandra C.
APPLICANT: McCherron, Alexandra C.
APPLICANT: McCherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 0705/5/144001
CURRENT APPLICATION UNMBER: U9/09/859,211
CURRENT FILING DATE: 2901-05-15
PRIOR APPLICATION UNMBER: 09/019,070
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION UNMBER: 08/862,445
PRIOR APPLICATION UNMBER: 08/862,445
PRIOR PILING DATE: 1997-04-28
PRIOR FILING DATE: 1997-04-28
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                  Sequence 35, Application US/09859211
Patent No. US2020157125A1
GENERAL INVORMATION:
GENERAL INVORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: MCPherron, Alexandra C.
APPLICANT: MCPherron, Alexandra C.
APPLICANT: MCPherron, Alexandra C.
APPLICANT: MCPherron, Alexandra C.
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Tocal Similarity
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Best Local (
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FILE REFERENCE: 07265/144001
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                                                                                                                                                                                                                                                                                                                                            82 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 130
                                                                                                                                                                                                                                                                                                                                                                                                  61 VHQANPRGSAGECCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 DEGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.1%;
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Pred. No. 4.4e-58;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR PELLING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
SEQ ID NO 8
LENGTH: 374
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CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION UNMEER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR FILING DATE: 1998-02-05
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR APPLICATION NUMBER: 08/947,910
PRIOR PILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/95,071
PRIOR FILING DATE: 1997-02-05
PRIOR PILING DATE: 1997-02-05
PRIOR PRIOR DATE: 1995-10-26
PRIOR PILING DATE: 1998-10-26
PRIOR PILING DATE: 1998-10-31
PRIOR PILING DATE: 1998-03-18
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR PILING DATE: 1993-03-19
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                                                                                                           Matches
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SEQ ID NO 35
LENGTH: 226
                                                                                                                                                            Query Match
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APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
FILE REFERENCE: JHU1470-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 177
266 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                            Local
                          1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVELQKYPHTHL 60
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                                                                                                                                  Similarity
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                                                                                                        Conservative
                                                                                                                               98.1%;
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98.2%;
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                                                                                                                            Score 618; DB 9; Length 374; Pred. No. 1.3e-57;
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                                                                                                        Mismatches
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; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-841-730-2
; ORGANISM: Porcine US-09-841-730-14
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US-09-841-730-14
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                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR FILING DATE: 1998-07-28
                                                                                                           PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09841730 Patent No. US20020157126A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
FILE REFERENCE: JHU1470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR APPLICATION NUMBER: 09/185,046
PRIOR PILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 09/185,046
PRIOR PILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR PILING DATE: 1998-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lee, Se-Jin AppLICANT: McPherron, Alexandra C.
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: McPherron, Alexandra C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: JHU1470-2
                                                     LENGTH: 375
TYPE: PRT
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APPLICANT: Lee, Se-Jin
APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
APPLICANT: McPherron, Alexandra C.
FITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR APPLICATION NUMBER: 08/867,910
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR FILING DATE: 1997-04-28
PRIOR FILING DATE: 1997-04-28
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US-09-841-730-18
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CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR FILING DATE: 1998-07-28
                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09859211 Patent No. US20020157125A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 18
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/054,461 PRIOR FILING DATE: 1997-08-01
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TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lee, Se-Jin APPLICANT: McPherron,
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nes 107; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.1%; Score 618; DB 9; Length 375; 98.2%; Pred. No. 1.3e-57; ative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 23
LENGTH: 375
                                                                                                                                                                                                                                        Matches 107;
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RESULT: 12
US-09-859-211-23
; Sequence 23, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
APPLICANT: McDherron, Alexandra C.
; APPLICANT: McDherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Gallus gallus US-09-859-211-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 07265/144001

CURRENT APPLICATION NUMBER: US/09/859,211

CURRENT FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: 09/019,070

PRIOR APPLICATION NUMBER: 09/019,070

PRIOR APPLICATION NUMBER: 08/862,445

PRIOR APPLICATION NUMBER: 08/847,910

PRIOR APPLICATION NUMBER: 08/847,910

PRIOR APPLICATION NUMBER: 08/795,071

PRIOR APPLICATION NUMBER: 08/795,071
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                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
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PRIOR APPLICATION NUMBER: 08/033,923
PRIOR FILING DATE: 1993-03-19
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PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR APPLICATION NUMBER: PCT/US94/03019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/033,923 PRIOR FILING DATE: 1993-03-19
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327 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
                                                                                                               267 DEGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
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                                        61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                              1 DFGLDCDEHSTESRCCRYPLIVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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98.2%;
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Pred. No. 1.3e-57;
                                                                                                                                                                                                                                                       Score 618; DB 9; Length 375; Pred. No. 1.3e-57;
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Sequence 27, Application US/09859211

Patent No. US2002015/125A1

GRINERAL INFORMATION:

APPLICANT: Lee, Se-Jin

APPLICANT: McPherron, Alexandra C.

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8

FILE REFERENCE: 07265/144001

CURRENT APPLICATION NUMBER: US/09/859,211

CURRENT FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: 09/019,070

PRIOR APPLICATION NUMBER: 09/862,445

PRIOR APPLICATION NUMBER: 09/862,445

PRIOR APPLICATION NUMBER: 09/867,445

PRIOR APPLICATION NUMBER: 09/867,45

PRIOR APPLICATION NUMBER: 09/867,765

PRIOR APPLICATION NUMBER: 09/
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                         CURRENT PAPLICATION UNMEER: US/09/859,211
CURRENT PILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR APPLICATION NUMBER: 08/95,071
PRIOR PILING DATE: 1997-02-05
PRIOR PILING DATE: 1997-02-05
PRIOR PILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR FILING DATE: 1993-03-19
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR FILING DATE: 1993-03-19
PRIOR FILING DATE: 1993-03-19
PRIOR FILING DATE: 1993-03-19
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NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/09859211
Patent No. US20020157125A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILING DATE: 1995-10-26
NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/033,923
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ilarity 98.2%;
Conservative
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; ORGANISM: Porcine US-09-859-211-29
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US-09-454-540-5
                                                                           US-09-454-540-5
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Ouery Match 98.1%; Score 618; DB 10; Length 375; Best Local Similarity 98.2%; Pred. No. 1.3e-57; Matches 107; Conservative 1; Mismatches 1; Indels
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: HALLE, PH.D., LISA A.
REGISTRATION UNMER: 38,347
REFERENCE/DOCKET UNMER: 0726
TELECOMOUNICATION INFORMATION:
TELEPHONE: 619/678-5070
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                                                                                                             PEATURE:
                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein IMMEDIATE SOURCE:
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APPLICATION NUMBER:
FILING DATE: Februar
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                                                                                                                                                 CLONE: GDF-8
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                                                                                            LOCATION:
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Local Similarity 98.2%;
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linear
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Sequence 4, Application US/09841730
Patent No. US20020157126A1
Patent No. US20020157126A1
PAPLICANT: Lee Se-Jin
APPLICANT: McCherron, Alexandra C.
ITILE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: ACONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
PILE OF INVENTION: NOUNEER: US/09/841,730
CURRENT APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR PILING DATE: 1996-07-28
PRIOR PILING DATE: 1996-08-01
NUMBER OF SEQ ID NOS: 29
SEPTIARE: FastSEQ for Windows Version 4.0
LENGTH: 376
TYPE: PRT
ORGANISM: Mus musculus
US-09-841-730-4
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Search completed: January 31, 2003, 18:27:18 Job time : 8 secs
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                                                                          61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
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Result
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Maximum DB seq length: 200000000
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Gapop 10.0 ,
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S01.352 Million cell updates/sec
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Match Length DB
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd
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    US-09-620-586B-12
US-09-620-586B-5
US-09-620-586B-11
US-10-251-115-2
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US-09-620-586B-2
US-09-620-586B-2
US-09-620-586B-3
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US-10-278-803-12
US-10-278-803-23
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US-09-620-586B-4
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US-09-620-586B-4
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US-10-278-803-12
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Sequence 12, Appli
Sequence 2, Appli
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Sequence 6, Appli
Sequence 22, Appli
Sequence 23, Appli
Sequence 24, Appli
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Sequence 3, Appli
Sequence 14, Appli
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US-09-620-586B-12
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                                     Sequence 5, Application US/09620586B

GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
TITLE OF INVENTION: Method for down-regulating GDF-8 activity
FILE REFERENCE: 3631-0117P
FULE REPERENCE: 3631-0117P
CURRENT FILING DATE: 2000-07-20
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 375
LENGTH: 375
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GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
TITLE OF INVENTION: Method for down-regulating GDP-8 activity
FILE REFERENCE: 3631-0117P
CURRENT APPLICATION NUMBER: US/09/620,586B
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 109
TWORE: NUMBER: US/09/620,586B
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NAME/KEY PEPTIDE
LOCATION: (1)..(109)
OTHER INFORMATION: Identical to residues 267-375 in
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        ORGANISM: Bos taurus
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US-10-278-803-8
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US-10-371-604A-6
US-09-871-604A-6
US-09-871-604A-6
US-09-871-604A-6
US-09-620-586B-15
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Pred. No. 9.9e-63;
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PRIOR FILING DATE: 1930-00-01-13
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 1997-07-14
PRIOR FILING DATE: 1997-07-14
PRIOR FILING DATE: 1997-07-761
PRIOR FILING DATE: 1998-01-15
PRIOR APPLICATION NUMBER: 05/01/1998-01-15
PRIOR FILING DATE: 1998-01-15
PRIOR FILING DATE: 1998-01-15
PRIOR FILING DATE: 1998-01-15
PRIOR FILING DATE: 1998-07-14
NUMBER: 0F SEQ ID NOS: 54
SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: Bos taurus
US-10-251-115-2
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US-09-620-586B-11
                                                                                                                                                                                                           Sequence 11, Application US/09620586B
GENERAL INFORMATION:
APPLICANT: MAE Biotech A/S
TITLE OF INVENTION: Method for down-regulating GDF-8 activity
FILE REFERENCE: 3631-0117P
CURRENT APPLICATION NUMBER: US/09/620,586B
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Grobet, Luc; Georges, Michel; and Poncelet, Dominique TITLE OF INVENTION: MUTATIONS IN THE MYOSTATIN GENE CAUSING DOUBLE-MUSCLING IN MAMMAI FILE REFERENCE: 52836/0016
CURRENT APPLICATION NUMBER: US/10/251,115
CURRENT FILING DATE: 2002-09-20
                                                                                                                               LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
            FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (1)...(109)

OTHER INFORMATION: Identical to residues 267-375 in SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375
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US-10-278-803-6
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APPLICATION NUMBER: US/10/278,803

EILING DATE: 22-Oct-2002

CLASSIFICATION: «Unknown»

PRIOR APPLICATION DATA:

APPLICATION UNMBER: US/09/451,501

FILING DATE: 30-NOV-1999

APPLICATION NUMBER: 08/795,071

FILING DATE: 18-March-1994

APPLICATION NUMBER: PCT/US94/03019

FILING DATE: 18-March-1994

APPLICATION NUMBER: PCT/US94/03019

FILING DATE: 18-March-1994

APPLICATION NUMBER: 93,347

REGISTRATION NUMBER: 39,347

REGISTRATION UNUMBER: 39,347

REGISTRATION THORWARTION:

TELEPHONE: 619/678-5070

TELEPHONE: 619/678-5070

TELEPHONE: 619/678-5099

INFORMATION FOR SEQ ID NO: 6:
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GENERAL INFORMATION:
APPLICANT: Se-Jin Lee et al.
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Best Local Similarity 98.2%;
Matches 107; Conservative
                                                                                                                                                                                                              Best Local Similarity 98.1
Matches 107; Conservative
                                                                                                                                                                                                                                                               Query Match
                              61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
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78 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 126
                                                                                                       18 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 77
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                                                                                                                                                                                                                                                                                                                                           IENGTH: 126 amino acids
TYPE: amino acid
TOPOLCGY: linear
MOLECULE TYPE: procein
FRACMENT TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0
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ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                        98.1%; Score 618; DB 6; Length 126;
98.2%; Pred. No. 2.5e-61;
ative 1; Mismatches 1; Indels
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                                                                                                                                                                                                              0; Gaps
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US-10-335-483-6; Sequence 6, Application US/10335483; GENERAL INFORMATION:

RESULT 6

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RESULT 7
US-09-620-586B-23
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Sequence 23, Application US/09620586B
GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
TITLE OF INVENTION: Method for down-regulating GDF-8 activity
FILE REFERENCE: 3631-0117P
CURRENT APPLICATION NUMBER: US/09/620,586B
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US/09/177,860

PILING DATE: -CURLOWN'S

APPLICATION NUMBER: 08/525,596

FILING DATE: 19-525-1995

APPLICATION NUMBER: PCT/US94/07762

FILING DATE: 08-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Wetherell, Jr., Ph.D, John R.

REGISTRATION NUMBER: 31,678

REFERENCE/DOCKET NUMBER: 07265/075001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                                                              61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Huynh, Thanh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                   VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 126
                                                                                                                                                                                                                                                                                                                                                                                            DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
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FILING DATE: 31-Dec-2002
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 618; DB 6; Length 126; Pred. No. 2.5e-61;
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                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/09620586B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: M&E Biotech A/S
TITLE OF INVENTION: Method for down-regulating GDF-8 activity
FILE REFERENCE: 3631-0117P
CURRENT APPLICATION NUMBER: US/09/620,586B
CURRENT FILING DATE: 2000-07-20
RUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                     LENGTH: 25
TYPE: PRT
                                                     LOCATION: (1)..(109)
OTHER INFORMATION: 109 C-terminal residues of human and bovine GDF-8
OTHER INFORMATION: (residues 267-375 in SEQ ID NO: 1)
                                                                                                                                                                                                                      NAME/KEY: SIMILAR
LOCATION: (110)..(124)
OTHER INFORMATION: Tet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (124)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SIMILAR
LOCATION: (52)..(160)
OTHER INFORMATION: Id
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(15)
OTHER INFORMATION: Identical to residues 216-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MUTAGEN
LOCATION: (37)..(51)
OTHER INFORMATION: T
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LOCATION: (16)..(36)
OTHER INFORMATION: T
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TYPE: PRT
                                                                                                                                                                     NAME/KEY: SIMILAR LOCATION: (125)..
                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial sequence
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                                                                                                       FEATURE:
NAME/KEY: SIMILAR
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                                  FEATURE:
                                                                                       OCATION:
                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                         FEATURE:
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DAME/KEY: SIMILAR
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                                                                                                                                                Diptheria toxoid P30 epitope (SEQ ID NO:
                                                                                                                                                                                                                            Tetanus toxoid P2 epitope (SEQ ID NO: 13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identical to residues 267-375 of SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetanus toxoid P30
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98.2%;
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Pred. No. 3.1e-61;
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; NAME/KEY: SITE
; LOCATION: (235)..(236)
; OTHER INFORMATION: Identical to (90)..(91)
US-09-620-586B-22
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GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
TITLE OF INVENTION: Method for down-regulating GDF-8 activity
FILE REFERENCE: 3631-0117P
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09871604A GENERAL INFORMATION:
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                                                                                                                                                                                              APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: LEE, Se-Jin
APPLICANT: LEE, Se-Jin
APPLICANT: MCHERERON, Alexandra C.
TITLE OF INVENTION: TRANSGENIC NON-HUMAN ANIMALS EXPRESSING A GDF-11 DOMINANT NEGATIVETITLE OF INVENTION: POLYPEPTIDE, AND METHODS OF MAKING AND USING SAME (Amended)
CURRENT APPLICATION NUMBER: US/09/871,604A CURRENT FILING DATE: 2001-05-31 PRIOR APPLICATION NUMBER: US 09/123,929 PRIOR FILING DATE: 1998-07-28 PRIOR APPLICATION NUMBER: US 09/019,901 PRIOR FILING DATE: 1998-02-06 PRIOR APPLICATION NUMBER: US 08/795,671 PRIOR FILING DATE: 1997-02-06
                                                                                                                                                                                  FILE REFERENCE: JHU1200-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Meleagris gallopavo
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LOCATION: (90)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 313
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Pred. No. 6.9e-61;
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                                                US-09-620-586B-3
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                                                                                                                        NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
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GENERAL INFORMATION:
APPLICANT: M&E Biotech A/S
TITLE OF INVENTION: Method for down-regulating GDF-8 activity
FILE REFERENCE: 3631-0117P
CURRENT APPLICATION NUMBER: US/09/620,586B
CURRENT FILING DATE: 2000-07-20
                                                                                                                                                                                                   Sequence 3, Application US/09620586B
GENERAL INFORMATION:
APPLICANT: MAE Biotech A/S
TITLE OF INVENTION: Method for down-regulating GDF-8 activity
FILE REFERENCE: 3631-0117P
CURRENT APPLICATION UNMERR: US/09/620,586B
CURRENT FILING DATE: 2000-07-20
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  Query Match
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PRIOR FILING DATE: 1996-09-03
PRIOR APPLICATION NUMBER: US 08/272,763
PRIOR FILING DATE: 1994-07-08
NUMBER OF SEQ ID NOS: 12
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SOFTWARE: Patentin Ver. 2.1
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                   ORGANISM: Gallus sp
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                                                                                                              ENGTH: 375
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98.2%;
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Pred. No. 7.1e-61;
    Score 618;
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Pred. No. 7.1e-61;
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    DB 5;
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Sequence 8, Application US/09620586B
; GENERAL INFORMATION:
; APPLICANT; MAE Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE; 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; CAGANISM: Sus scrofa
US-09-620-586B-8
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US-10-278-003-14
US-10-278-003-14
; Sequence 14, Application US/10278803
; GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VHQANPRGSAGPCCTPTXMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                      ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING YSTEM: Windows95

SOFTWARE: FEATSEO for Windows Version 2.0
                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/451,501
PILING DATE: 30-Nov-1999
APPLICATION NUMBER: 08/795,071
FILING DATE: CUDAINOMAN
APPLICATION NUMBER: PCT/US94/03019
PILING DATE: 18-March-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Se-Jin Lee et al.,
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,803
FILING DATE: 22-Oct-2002
CLASSIFICATION: -Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
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    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 618; DB 5; Length 375; Pred. No. 7.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/10278803 GENERAL INFORMATION:
                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/451,501

PILING DATE: 30-Nov-1999

APPLICATION NUMBER: 08/795,071

PILING DATE: UB:Norm

APPLICATION NUMBER: PCT/US94/03019

PILING DATE: 18-March-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lisa A. Haile, Ph.D.

REGERENCE/DOCKET NUMBER: 07265/105001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

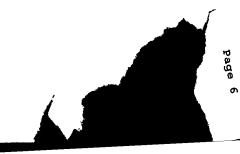
SOFTWARE: PASESSO for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 072
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,803
FILLING DATE: 22-Oct-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Se-Jin Lee et al.,
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS: 7
CORRESPONDENCE ADDRESS: 8
ADDRESSES Fish & Richardson P.C.
ADDRESSES: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA.
STATE: CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 618; DB 6; Length 375; Pred. No. 7.1e-61; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07265/105001
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밁

В

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CLONE: Baboon GDF-8

| RAME/KEY: Protein | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1...375 | 1..
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Minimum DB seg length: 0
Maximum DB seg length: 200000000
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                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
       SPTREMBL 21:*
1: sp_archea:*
2: sp_bacteria:
3: sp_funga:*
4: sp_numan:*
5: sp_inverteb:
6: sp_manmal:*
7: sp_mhc:*
8: sp_organell
9: sp_plant:*
10: sp_plant:*
11: sp_volent:
12: sp_virus:*
11: sp_volent:
12: sp_virus:*
13: sp_vertebx:
14: sp_unclass:
14: sp_unclass:
15: sp_racheap:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-620-586B-12
630
1 DFGLDCDEHSTESRCCRYPL......BGQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           671580 seqs, 206047115 residues
sp_invertebrate:*
sp_mammal:*
sp_mhammal:*
sp_mhamele:*
sp_organele:*
sp_phate:*
sp_vertebrate:*
sp_vertebrate:*
sp_unclassified:*
sp_unclassified:*
sp_archeap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                  sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                            671580
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	

45	44	43	42	41	40	39	38	37	36	(J)	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
223.5		•	٠	٠	٠		243.5		244.5	245	257	259	286	299.5	299.5	302	311	394	521	532	543	546	4	551	552	553	553	553
•	•		•	٠	•	٠		•	•	38.9	٠	٠						•	82.7	٠	86.2	86.7			87.6			
361	349	354	138	115	115	115	392	393	115	395	370	263	58	598	598	104	191	78	107	359	96	373	377	376	373	376	376	376
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096504	097138	Q9YGV1	Q9W6T9	Q9DGE6	Q9DGF0	Q9DGF1	Q9PWR8	Q90261	Q9DGE9	Q9PWG6	Q91350	Q8QH11	Q95MF3	Q9V4F4	Q9XZ62	Q90Z79	Q98TY4	Q9XS86	Q9BG54	Q8QG53	Q9W759	Q98UB3	Q98TB3	Q90W06	Q90W17	Q90WC8	Q90WC9	Q98TB4
O96504 branchiosto	O97138 brugia mala							Q90261 brachydanio		anguilla		. umbrina	Q95mf3 sus scrofa		a.	Q90z79 ictalurus p	4		Q9bg54 sus scrofa	Q8qg53 sparus aura	Q9w759 cairina mos	salvel	ω	Q90w06 umbrina cir	salmo s	Q90wc8 morone ame	Q90wc9 morone saxa	Q98tb4 oreochromis

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002400; GF cysknot.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF000019; TGF-beta; 1.
Pfam; PF00688; TGFb propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                     Q9GM97;
Q9GM97;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9TSY2;
Hosoyama T., Yamanouchi K., Tojo H., Tachi C.;
"Molecular cloning of equine myostatin cDNA and serum level of
myostatin in horse.";
                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic organization, sequence and polymorphism of myostatin (GDF8; MSTM) gene."; Anim. Genet. 30:468-470(1999).
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; AJ237920; CAB40844.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9823;
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                           Myostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stratil A., Kopecny M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myostatin (Fragment).
                                                                            SEQUENCE FROM N.A.
STRAIN=THROUOGHBRED;
                                                                                                                                                      NCBI_TaxID=9796;
                                                                                                                                                                                                                                      Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P18075; 1BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20078370; PubMed=10612246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQXYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 1
162 AA; 18290 MW;
                                                                                                                                                                                                                                                                                                               1 (TrEMBLrel. 16,
1 (TrEMBLrel. 16,
2 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 618; DB 6;
Pred. No. 2.8e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FE3535334512856E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                    Matches
                                                                                                                                               Query Match
                                                                                                                                                                                                    InterPro; IPR0012048; EP-hand.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb propeptide; 1.
ProDom; PD000357; TGFb; I.
PROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002048; EF-hand.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb.N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb propeptide; 1.
ProDom; PD000357; TGFb; 1.
SWART; SM00204; TGFB; 1.
PROSITE; PS00018; EF HAND; UNKNOWN 1
PROSITE; PS000250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q95J86;
Q95J86;
01-DEC-2001
                                                                                                                                                                           Glycoprotein.
SEQUENCE 37
                                                                                                                                                                                                                                                                                                                              Mayostatin.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein.
SEQUENCE 375 AA; 42736 MW; 6F424ECBEE4D9936 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-- SIMILARIY: BELONGS TO THE TGF-BETA FAMILY.
EMBL, AB033541, BAB16046.1;
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HSSP, P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Macaca.
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                          267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                            61
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                                                                                                                                  Local
                                                                                   1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                          VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                    107;
                                                                                                                                                                                                                                                                                                                                                                                                                       =GASTROCNEMIUS;
                                                                                                                                  Similarity
                                                                                                                                                                           375 AA; 42722 MW; 2149B46AC7D446E7 CRC64;
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.1%;
                                                                                                                                98.2%;
                                                                                                                                                 98.1%;
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    Mismatches

    Mismatches

                                                                                                                                Score 618;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 618; DB 6;
Pred. No. 6.5e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375
                                                                                                                                                 DB 6; Length 375;
                                                                                                                                  .5e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                   1; Indels
 375
                                                                                                                    0;
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                                                                                                                    Gaps
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RESULT 6
Q8UWD7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                         Q8UWD7;
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8UWD8
Q8UWD8;
Q1-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
Duck, Goose, Pigeon and Quail.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF440864; AALJS278.1;
InterPro; IPR001038; TGF-band.
InterPro; IPR0010383; TGFb.
InterPro; IPR0011833; TGFb. N.
Pfam; PF00088; TGF-beta; 1.
Pfam; PF00088; TGF-by propeptide; 1.
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00019; TGF-beta; 1.
Pfam; PF00088; TGFb propeptide; 1.
Probom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS00050; TGF BETA 1; UNKNOWN 1.
PROSITE; PS00050; TGF BETA 1; UNKNOWN 1.
PROSITE; PS00050; TGF BETA 1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Gu Z., Yang W., Cheng Z., Li H., Zhu D.;

"Molecular Cloning and Tissue Distribution of the Myostatin Gene
                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
"Molecular Cloning and Tissue Distribution of the Myostatin Gene
Duck, Goose, Pigeon and Quail.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF440863; AAL35277.1; -.
                                                                                                                                                                                                                                                  Coturnix chinensis.
                                                                                                                                                                                                                                                                                                                                                        QBUWD7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002048; EF-hand.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myostatin.
                                                                                                                                                                                      NCBI_TaxID=46218;
                                                                                                                                                                                                                     Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                             Myostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                         19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                             VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                          VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                     Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
a; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.1%; Score 618; DB 13; 98.2%; Pred. No. 6.5e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88296FOAE779476E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13; Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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01-MAR-2002 01-MAR-2002 01-JUN-2002

(TrEMBLrel. 20, (TrEMBLrel. 20, (TrEMBLrel. 21,

Last sequence update)
Last annotation update)

Created)

GRUWD9;

6dMD8

PRELIMINARY;

375 AA.

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RESULT 7

Q98SPO
ID Q98S
AC Q9
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                                                                                                                                                                                                                                                                                   Matches 106;
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

EMBL, AF346599, AAK18000.1; -.

HSSP; P18075; 1BMP.

InterPro; IPR002048; EF-hand.

InterPro; IPR001399; TGFb.

InterPro; IPR001111; TGFb.N.

Pfam; PF00688; TGFb propeptide; 1.

Pfam; PF00688; TGFb propeptide; 1.

ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q98SP0;
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PROSITE; PS00210; EF HAUD; UNKNOWN 1.

PROSITE; PS00250; TGF HETA 1; UNKNOWN 1.

SEQUENCE 375 AA; 42721 MW; B893B11A42DE0725 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00018; EF HAND; UNKNOWN 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang Y., Yang W., Zhu D.; "Genomic structure and expression of the chicken GDF-8 during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9031;
                                                                                                                                     EQUENCE FROM N.A.
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327 VHOANPRGPAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                           61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 98.1%; Score 618; DB 13; Length 375; Similarity 98.2%; Pred. No. 6.5e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                        375 AA; 42717 MW; D980E286426E4D4F CRC64;
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                      97.3%; Score 613; DB 13; Length 375; 97.2%; Pred. No. 2.5e-63;
                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375
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                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                       Gaps
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RESULT 9
Q8UWE0
                                                                             Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8UWEO;
Q8UWEO;
01-MAR-2002
                                                                                                                                                                                                               Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
"Molecular Cloming and Tissue Distribution of the Myostatin Gene
Duck, Goose, Pigeon and Quail.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF440861; AAL35275.1;
InterPro; IPR002048; EF-hand.
InterPro; IPR001139; TGFb N.
InterPro; IPR001139; TGFb N.
InterPro; IPR001111; TGFb N.
Pfam; PF00068; TGFb Droppeptide; 1.
EMART; SM00204; TGFB; 1.
EMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myostatin.
MSTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002048; EF-hand.
InterPro; IPR001839; TGFb.
InterPro; IPR001813; TGFb.
InterPro; IPR00111; TGFb N.
Pfam; PP00688; TGFb beta; 1.
Prompt PP00688; TGFb propeptide; 1.
Proscom; PD000357; TGFb; 1.
PROSITE; PR00204; TGFB; 1.
PROSITE; PR00204; TGFB BETA 1; UNKNOWN 1.
PROSITE; PS00250; TGF BETA 1; UNKNOWN 1.
PROSITE; PS00250; TGF BETA 1; UNKNOWN 1.
                                                                                                                                                                   PROSITE; PS00018; EF HAND; UNKNOWN 1.
SEQUENCE 375 AA; 42817 MW; 1BA7FF5225C23620 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anas platyrhynchos (Domestic duck).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves; Neognathae, Anseriformes, Anatidae, Anas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duck, Goose, Pigeon and Quail.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF440862; AAL35276.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anser anser (domestic goose).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Anseriformes, Anatidae, Anser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gu Z., Yang W., Cheng Z., Li H., Zhu D., Molecular Cloning and Tissue Distribution of the Myostatin Genewholecular Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCFGECEFVFLQKYPHTHL 326
                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVPLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106;
                                                                             106;
                                                                                                       Similarity
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                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.1%;
97.2%;
                                                                           96.8%; Score 610; DB 13; Length 375; 97.2%; Pred. No. 5.6e-63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 612; DB 13;
Pred. No. 3.3e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                           0;
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RESULT 11
Q9MZ18
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Q95N11
ID Q95N1
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q95N11 PRELIMINARY;
Q95N11;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
Myostatin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein.
NON_TER
NON_TER 18
           Lian Z., Jin H., Li N.;
"Cloning of intron 2 of the myostatin gene in sheep.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ database
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                          Q9MZ18;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Boyidae; Caprinae; Capra.
Boyidae; Caprinae; Capra.
NCBI_TaxID=9925;
                                                                                                                                                                                                            Ovis aries (Sheep).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Ceta
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9MZ18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AY032689; AAK49790.1; -.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGFb-beta; I
Pfam; PF00688; TGFb propeptide; 1.
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
EMBL; AF266758; AAF78069.1;
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                     Myostatin (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capra hircus (Goat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 VHQANPKGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPGMVVDRCG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSEECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VHQANPRGSAGPCCTFTKMSPINMLYFNGEGQIIYGKIPAMVVDRCG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VHQANPRGSAGECCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFLFLQKYPHTHL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 AA;
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185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185
20953 MW;
                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.4%;
                                                                                                                                                                                                                                                                                                                                                                          15,
15,
21,
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Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 595; DB 6; Length 185; Pred. No. 1.5e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03675B386E9D64D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185
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                                                     databases
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HSSP; P12643; 3BMP

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RESULT 13
Q90W05
ID Q90W0
AC Q90W0
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Q90YY0
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                                                                                                                                            Matches
                                                                                                                                                     Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                      Q90YYO PRELIMINARY; Fr., Q90YYO PRELIMINARY; Fr., Q90YYO D.-DEC-2001 (TrEMBLrel. 19, Created) O1-DEC-2001 (TrEMBLrel. 19, Last seq O1-JUN-2002 (TrEMBLrel. 21, Last ann
 Q90W05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein.
NON_TER
NON_TER 18
                                                                                                                                                                                                  InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb.N.
Pfam; PF000019; TGFb-beta; I.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                             Ictalurus punctatus (Channel catfish).

Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;

Ictaluridae; Ictalurus.
                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                            Glycoprotein.
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00250;
                                                             343
                                                                                                 283 GLDCDENSSESRCCRYPLTVDFEDFGWDWIIAPKRYKANYCSGECDYVHLQKYPHTHLVN 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 VHQANPKGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPGMVVDRCG 185
                                                                               63
                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 93.3%;
Local Similarity 94.4%;
                                                                                                              1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                    QANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCG 107
                                                          KANPRGTAGPCCTPTKMSPINMLYFNGKEQIIYGKIPSMVVDRCGCS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFGLDCDVHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFLFLQKYPHTHL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101;
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                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185
185 AA;
                                                                                                                                                                                  389 AA; 43600 MW; 569FB952B7E9E173 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
          PRELIMINARY;
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                    Liu Z.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185
; 20923 MW; BA9634203A552850 CRC64;
                                                                                                                                                  88.7%;
                                                                                                                                         9;
                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                   Score 559; DB 13; Length 389; Pred. No. 5.2e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 588; DB 6,
Pred. No. 1e-60;
          PRT;
                                                                                                                                          Mismatches
         385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
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                                                                                                                                         0
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PER PROPERTY OF STREET OF 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O9DD18 PRELIMINARY; PRT; 373 AA.

O9DD18;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-CT-2001 (TrEMBLrel. 18, Last sequence update)
O1-UN-2002 (TrEMBLrel. 21, Last annotation update)
"The two myostatin genes of Atlantic salmon (Salmo salar) are expressed in a variety of tissues.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.

"The two myostatin genes of Atlantic salmon (Salmo salar) are expressed in a variety of tissues.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmo salar (Atlantic salmon).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Butinopterygii; Neopterygii; Teleostai; Buteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myostatin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein.
SEQUENCE 385 AA; 43704 MW; 18F902CE325A3916 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000357; TGFb; 1.
PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb propeptide; 1.
ProDom; PD000357; TGFb; 1.
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neoteleostei;

Actinopterygii, Neopterygii, Telaostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                         Andersen O.;
                                                                                                              SEQUENCE FROM N.A.
OSTDYP T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.,
                                                                                                                                                                                                               Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Andersen O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patarnello T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maccatrozzo L., Bargelloni L., Radaelli G., Mascarello F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CBI_TaxID=8175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 VNKANPRGSAGPCCTPTKMSPINMLYFNRKEQIIYGKIPSMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 DSGLDCDENSPESRCCRYPLTVDFEDFGWDWIIAPKRYKANYCSGECEYMHLQKYPHTHL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _TaxID=8030;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 556; DB 13;
Pred. No. 1.1e-56;
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                                                                                                                               Query Match 87.8%; Score 553; DB 13; Length 373; Best Local Similarity 87.2%; Pred. No. 2.5e-56; Matches 95; Conservative 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 87.8%; Score 553; DB 13; Length 373; Best Local Similarity 87.2%; Pred. No. 2.5e-56; Matches 95; Conservative 8; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; AJ297267; CAC19541.2; -.
EMBL; AJ15606; CAC19700.1; -.
HSSP; P12643; 3BMP.
InterPro; IPRO01839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00019; TGF-beta; I.
SMART; SM00204; TGFB; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Rescan P.-Y., Jutel I., Ralliere C.;
Rescan P.-Y., Jutel I., Ralliere C.;
"Two myostatin genes are differentially expressed in myotomal muscle
of the trout (Oncorhynchus mykiss).";
J. Exp. Biol. 0:0-0(2001).
-!-SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; AF273035; AAK717077.1; -.
INTERPRO; IPR001139; TGFB.
InterPro; IPR00111; TGFB N.
Pfam; PF00688; TGF-beta; I.
Pfam; PF00688; TGF-beta; I.
PROSITE; PS000357; TGF-BETA_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myostatin 1.

Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Actinopterygii, Neopterygii, Teleostei; Euteleostei;

Protaganthopterygii, Salmoniformes, Salmonidae, Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0902D2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                             Glycoprotein.
SEQUENCE 373 AA; 42049 MW; \9DD4771B5CF671EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q90ZD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 VNKANPRGTAGECCTPTKMSPINMLYPNRKEQIIYGKIPSMVVDRCGCS 373
                                                                 265 DSGLDCDENSPESRCCRYPLTVDFEDFGWDWIIAPKRYKANYCSGECEYMHLQKYPHTHL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 DSGLDCDENSPESRCCRYPLTVDFEDFGWDWIIAPKRYKANYCSGECEYMHLQKYPHTHL 324
                     61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                      1 DFGLDCDEHSTESRCCRYPLIVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 373 MYOSTATIN.
373 AA; 41896 MW; C641D71D83E66C4D CRC64;
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Search completed: January 31, 2003, 18:21:08

Job time : 25 secs

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Maximum Match 100%
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Copyright (c) 1993 - 2003 Compugen Ltd.
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IHBB BOVIN
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homo sapien
bos taurus
brachydanio
rattus norv
homo sapien
mus musculu
equus cabal
caenorhabdi
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bos taurus
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sus musculu
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InterPro; IPRO0111; TGFb.
Pfam; PF00019; TGF-beta; I
Pfam; PF00688; TGF-beta; I
ProDom; PD000357; TGFb; 1.
SMART; SW00204; TGFb 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDF8 CHICK STANDARD;
042220;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
16-OCT-2001 (Rel. 40) Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
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This SWISS-PROT entry is copyright. It is produced throubetween the Swiss Institute of Bioinformatics and the
                                                                                                                                          McDherron A.C., Lee S.-J.;
"Double muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDF8 OR MSTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHICK
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                                                                                                                                                                                                                                         STRAIN=White leghorn; TISSUE=Skeletal muscle; MEDLINE=98024153; PubMed=9356471;
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                      Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267
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                                                                         SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SI SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                           MUSCLE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; AF019620; AAB
; AF320998; AAG
; P18075; 1BMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109;
                                                                                                                                                                                                                                                                                                                                                                                                                                     gallus (Chicken).
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Weognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 630; DB 1; 100.0%; Pred. No. 5.3e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Signal; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL:

POTENTIAL:

GROWTH/DIFFERENTIATION FACTOR
BY SIMILARITY.

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INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTEN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tation update)
precursor (GDF-8) (Myostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                       It is produced through
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                                                               MEDLINE=99061972; PubMed=9843994;
Gonzalez-Cadavid N.F., Taylor W.E., Yarasheski K., Sinha-
Gonzalez-Cadavid N.F., Taylor W.E., Yarasheski K., Sinha-
Ma K., Ezzat S., Shen R., Lalani R., Asa S., Mamita M., N
Arver S., Bhasin S.;
Arver S., Bhasin S.;
Paroc S., Bhasin S.;
Proganization of the human myostatin gene and expression
"Organization of the human myostatin gene and expression"
"Organization of the human myostatin gene and expressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         014793;
15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
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CARBOHYD
                                                                                                                                                                                                                                                                                                            TISSUE=Skeletal muscle;
MEDLINE=98024153; PubMed=9356471;
McPherron A.C., Lee S.-J.;
"Double muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
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InterPro; IPRO01111; TGFb N.
Pfam; PF00019; TGFb-beta; I.
Pfam; PF00688; TGFb propeptide; 1.
ProDom; PD000357; TGFb; 1.
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-!- SUBUNIT: HOMODIMER;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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                                                                                                                                                                                                                                                      TISSUE≃Muscle;
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                              MUSCLE GROWTH.
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SM00204; TGFB; 1.
SM00204; TGF_BETA_1;
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1 23 POTENTIAL
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  HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY)
Y: BELONGS TO THE TGF-BETA FAMILY.
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98.2%;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . . ) (POTENTI)
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Pred. No. 1
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       RESULT 4
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                       042221;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRU01131; TGFb N.
InterPro; IPR001111; TGFb N.
Pfam; PF00698; TGFb propeptide;
Prondom; PF00698; TGFb; 1.
Prondom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC: 4223; GDF8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF019627; AAB86694.1; -. EMBL; AF104922; AAC96327.1; -.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                           Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
                                                                                                                                                                                                                                                                                                                                                                     Growth/differentiation factor 8 precursor (GDF-8) (Myostatin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MELGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00204; TGFB;
                                                                                                                             MEDLINE=98024153; PubMed=9356471;
McDherron A.C., Lee S.-J.;
McDherron A.C., Lee S.-J.;
McDhermuscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).

-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                     GDF8 OR MSTN
                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDF8 MELGA
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                                                                         -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                       TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VHQANDERGSAGPCCTPTXMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DFGLDCDEHSTESRCCRYPLTVDFBAFGWDWIIAPKRYKANYCSGECEFVFLQXYPHTHL 60
                                                                                                                 MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00250;
                                                                                                                 GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
267
281
309
313
339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50; TGF BETA 1; 1.
Cytokine; GTycoprotein; Signal.
23
POTENTIAL.
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375
340
372
374
339
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98.2%;
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GROWTH/DIFFERENTIATION FACTOR 8.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 618;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EBFF6129725E6AFA CRC64;
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                       a collaboration - MBL outstation -
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RESULT
GDF8_P1
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Best Local
                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
MEDLINE=98024153; PubMed=9356471;
MEDLINE=98024153; PubMed=9356471;
MCPherron A.C., Lee S.-J.;
MCPherron A.C., Lee S.-J.;
"Double muscling in cattle due to mutations in the myostatin gene.";
"Double muscling in cattle due to mutations in the myostatin gene.";
"Double muscling in cattle due to mutations in the myostatin gene.";
"Double muscling in cattle due to mutations in the myostatin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O1831;
O1831;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPROULDS; TGFb N. InterPro; IPRO01111; TGFb N. Pfam; PF000019; TGFb propeptide; PF00688; TGFb propeptide; Pf0688; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth factor; Cytokine; Glycoprotein; Signal. SIGNAL 1 23 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF019625; AAB86692.1; ALT_INIT. HSSP; P18075; 1EMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                         Daneau I., Silversid
Submitted (SEP-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                     Voelker G.R., Conroy
                                                                                                                                                                                                                                                                        rissue=skeletal muscle;
                                                                                              CISSUE=Muscle;
                                                                                                                          SEQUENCE OF 1-10 AND 36-375 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267
                                                                                                                                                                          ubmitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                         Porcine myostatin cDNA sequences: Duroc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
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MUSCLE GROWTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                     Silversides D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                      B) to the EMBL/GenBank/DDBJ
SPECIFICALLY AS A NEGATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.1%;
98.2%;
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                                                                                                                                                                                                                                                     J.C., Wheeler M.B.;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 618; DB 1;
Pred. No. 1.2e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suina; Suidae;
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                                                                                                                                                                                                                            Hampshire, Meishan
                      databases
REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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                           ဝ္ပ
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                           SKELETAL
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RESULT 6
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DISULFID
DISULFID
DISULFID
                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                        GDF8 OR MSTN.
Mus musculus (Mouse)
                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 8 precursor (GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF019623; AAB86690.1; --
EMBL; AF188635; AAF02771.1; --
EMBL; AF188636; AAF02772.1; --
EMBL; AF188637; AAF02772.1; --
EMBL; AF188638; AAF02773.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
       Nature 387:83-90(1997).
                                       MEDLINE=97284412; PubMed=9139826; MCPherron A.C., Lawler A.M., Lee S.-J.; WCPherron of skeletal muscle mass in mice by superfamily member.";
                                                                                                                                                                                                                                                             GDF8_MOUSE
                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth factor; Cytokine; Glycoprotein; Signal. SIGNAL 1 23 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb propeptide; 1.
ProDom; PD000357; TGFb; 1.
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                             327
                                                                                                                                                                                                                                                                                                                                                                                               267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                          MUSCLE GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                    DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                    107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF093798; AAC
P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; PD000357; TGFb; 1.
SM00204; TGFB; 1.
E; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                             TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC08035.1; -.
AAC62489.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42791 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GROWTH/DIFFERENTIATION FACTOR
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 618; DB 1;
Pred. No. 1.2e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                  Sciurognathi; Muridae;
                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF658685EFDA3418 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                           376
                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                        (GDF-8)
                                                    a new TGF-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                       (Myostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                   Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
InterPro; IPR001111; TGFb N.
Pfam; pP00019; TGF-beta; I.
Pfam; pP00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
SMART; SW00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                             GDF8 RAT STANDARD; PRT; 376 AA.
035312;
15-UTL-1999 (Rel. 38, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
16-UTL-1991 (Rel. 40, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8) (Myostatin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND ADULT
- SKELETAL MUSCLE. WEAK EXPRESSION IN ADIPOSE TISSUE.
-!- DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-CONTUM IN
ONE-THIRD OF DEVELOPING SOMITES. AT DAY 10.5, EXPRESSED IN THE
MYCTOME COMPARTMENT OF SOMITES. AT LAY 10.5, EXPRESSED IN THE
MYCTOME COMPARTMENT OF SOMITES. AT LAY 10.5, EXPRESSION
DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION
                                                                                 TISSUE=Skeletal muscle;
MEDLINE=98024153; PubMed=9356471;
McPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                         GDF8 OR MSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Growth factor; Cytokine; Glycoprotein; Signal. SIGNAL 1 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U84005; AAC53167.1; -. HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                    "Double muscling in cattle due to mutations in the myostatin gene.".
Proc. Natl. Acad. Sci. U.S. A. 94:12457-12461[1997].
                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Skeletal mu
                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
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                                                                                                                                                                                                                                       NCBI_TaxID=10116
(- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VHQANDRGSAGECCTETKMSFINMLYFNGEGQIIYGKIFAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONTINUES IN ADULTHOOD. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 618; DB 1;
Pred. No. 1.2e-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (PO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GROWTH/DIFFERENTIATION FACTOR BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3E19814DD62C08BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                    MEDLINE=98074153; PhbMed=9356471;
McPherron A.C., Lee S.-J.;
"Double muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl Acad. Sci. U.S.A. 94:12457-12461(1997).
Proc. Natl Acad. Sci. U.S.A. 94:12457-12461(1997).
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                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb_propeptic
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE≃Skeletal mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000357; TG
SMART; SM00204; TGFB
                                                                                                                                                                                                                                                Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                             Papio hamadryas (Hamadryas baboon)
                                                                                                                                                                                                                                                                                                                GDF8 OR MSTN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P18075;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                             -!- SUBUNIT: HOMODIMER; DISULPIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                  MUSCLE GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUSCLE GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00250; TGF_BETA 1; 1.
actor; Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                            muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _propeptide; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42829 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.1%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 618;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GROWTH/DIFFERNITIATION FACTOR 8. BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLONAC. . .) (POTENTIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                 375
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                                                                                                                                                                                                                                                                                                                                                                                                               A
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; traveller, 1. Pfam; PF00019; TGF-beta; 1. Pfam; PF00688; TGFb propeptide; Pfam; PF00688; TGFb; 1.
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                                                                                                                                                                    MEDLINE=98024153; PubMed=9356471;
McPherron A.C., Lee S.-J.;
McPherron A.C., Lee S.-J.;
McDuble muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S. A. 94:12457-12461(1997).
-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL MUSCLE GROWTH.
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                              15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
16-UCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                      GDF8 OR MSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    018830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF019619; AAB86686.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                      TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P18075; 1BMP
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECBFVFLQKYPHTHL 60
                                                                                                                                       SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY). SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFGLDCDEHSTESRCCRYPLTVDFEALGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytokine; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.1%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42688 MW;
                                                                                                                                                                                                                                                                                                                                                      Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 612; DB 1;
Pred. No. 5.4e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GROWTH/DIFFERENTIATION FACTOR 8.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7B49B90ACAB926EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٧.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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EMBL;

PROPEP SIGNAI

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Matches 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDFB_MOUSE STANDARD; PRT; 405 AA.
92XIM4; 096X55; Q9R221;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 11 precursor (Bone morphogenetic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
DISULFID
DISULFID
                            SEQUENCE OF 75-405 FROM N.A.

MEDILINE=99173787; PubMed=10072786;

Nakashima M., Toyono T., Akamine A., Joyner A.;

"Expression of growth/differentiation factor 11, a new member of members of members of members of members of members of members of members.";

Mech. Dev. 80:185-189(1999).
                                                                                                                                                                                  MEDLINE-99318097; PubMed=10391213; McPherron A.C., Lawler A.M., Lee S.-J.; McPherron of anterior/posterior patterning of the axial skeleton growth/differentiation factor 11.";
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=99177155; PubMed=10075854;

Gamer L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDF11 OR BMP11.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000357; TGFB;
SMART; SM00204; TGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
pronom: PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                        STRAIN=129/SvJ
                                                                                                                                                                                                                                                                                                              Dev. Biol. 208:222-232(1999).
                                                                                                                                                                                                                                                                                                                             "A novel BMP expressed in developing mouse limb, spinal cord, and tail bud is a potent mesoderm inducer in Xenopus embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 VHQANPKGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPGMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                      FUNCTION:
  IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P18075; 1BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF019622; AAB86689.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 AA;
                                                                                                                                                                  22:260-264(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                        SECRETED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.5%;
                  SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Signal.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERCHAIN (BY SIMILARITY).

N-LINESD (GLCNAC. . .) (POTENTIAL).

N-LINESD (GLCNAC. . .) (POTENTIAL).

; 1C36F3833BB11241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred
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GROWTH/DIFFERENTIATION FACTOR
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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1.5e-60;
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 375;
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                                                        GDFB
                                                                           RESULT 11
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                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                            Matches
GDFB HUMAN STANDARD;

095390; Q9UID1; Q9UID2;

16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SN
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.

-!- SUBUNIT: HOMOLIMER, DISCULFIDE-LINKED (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Secreted (Probable).

-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD, INITIALLY DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALIZING TO REGIONS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADULT DENTAL FULL AND BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF100906; AAC72853.1; --
EMBL; AF100904; AAC72853.1; JOINED.
EMBL; AF109905; AAC72853.1; JOINED.
EMBL; AF028337; AAF21633.1; --
EMBL; AF028335; AAF21633.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb propepti
                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1338027;
                                                                                                                                                  61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: FIRST STRONGLY EXPRESSED IN RESTRICTED DOWALNS AT 8.5 DAYS POST COTTUS (DPC) WHERE IT IS HIGHEST IN THE DOWALNS AT 10.5 DPC, EXPRESSED IN THE BRANCHIAL ARCHES, LIMB BUD, TAIL BUD AND POSTERIOR DORSAL NEURAL TUBE. LATER, EXPRESSED IN TERMINALLY-DIFFERENTIATED ODONTOBLASTS, THE NASAL EPITHELIUM, RETINA AND SPECIFIC REGIONS OF THE BRAIN.
RETINA AND SPECIFIC REGIONS OF THE BRAIN.
                                                                                                                              VQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPGMVVDRCGCS 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF092734;
P18075; 1
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                                                                                                                                                                                                                                                                          97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00204; TGFB;
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          00688; TGFb_propeptide; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00250;
                                                                                                                                                                                                                                                                                                                                               405 AA;
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD05267.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gdf11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGF_BETA
                                                                                                                                                                                                                                                                                                                                                 44946 MW;
                                                                                                                                                                                                                                                                                          91.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                          Score 573;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
B -> G (IN REF. 3).
T -> N (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GROWTH/DIFFERENTIATION FACTOR 11.
                                                                                                                                                                                                                                                                                                                                                 A74E382710A14781 CRC64;
                                                                                                                                                                                                                                                                            Mismatches
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267

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GDFB RESULT 10

MOUSE

Mech.

407 AA.

.3e-56; DB 1;

Length 405; Indels

٥, Gaps

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SOCOCORPARA A REPRESENTATION OF THE PROPERTIES O
                        δ
                                                                   Query Match
Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                               Pfam; PF00688,

Pfam; PF00688,

ProDom; PD000357; TGF2,

SMART; SM00204; TGFB; 1.

PROSITE; PS00250; TGF_BETA 1; 1.

PROSITE; PS00250; TGF_BETA 1; 1.

POTENTIAL.

POTENTIAL.

POTENTIAL.

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15-JUN-2002
                                                                                                                                                                                                          DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT. PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
-!- SUBUNIT: HOMODIMER; DISULPIDE-LINKED (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99318097; PubMed=10391213; McPherron A.C., Lawler A.M., Lee S.-J.; McPherron A.C., Lawler A.M., Lee S.-J.; The state of the axial skeleton "Regulation of anterior/posterior patterning of the axial skeleton growth/differentiation factor 11."; Nat. Genet. 22:260-264 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fetal brain;
MEDLINE=99177155; PubMed=10075854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDF11 OR BMP11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia;
                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001839; TGFb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   novel BMP expressed in developing mouse limb, spinal cord, and
1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        603936; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is a potent
Biol. 208:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00019; TGF-beta; 1.
PF00688; TGFb propeptide;
PF00688; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF100907; AAC72852.1; -. AF028333; AAF21630.1; -. AF028334; AAF21631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L.W., Wolfman N.M.,
                                                                     Similarity
97; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC: 4216; GDF11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208:222-232 (1999)
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210
313
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                                                                        Conservative
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Last annotation update)
n factor 11 precursor (Bone morphogenetic protein
                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Celeste A.J., Hattersley G., Hewick
                                                                                                                                                                                                       GROWTH/DIFFERENTIATION FACTOR 11.
POLY-ALA.
POLY-GLY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                   Score 573; DB Pred. No. 1.3e 7; Mismatches
                                                                     7;
                                                                                                                                                                                        N-LINKED (GLCNAC.
                                                                                                                                                               E8FF48E363635BA8 CRC64;
                                                           DB 1;
1.3e-56;
5;
                                                                                                             Length 407
                                                                        Indels
                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restrictions on
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EMBL outstation -
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98024153; PubMed=9356471;
McDherron A.C., Lee S.-J.;
WCDholle muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, 30-MAY-2000 (Rel. 39, 15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDF8
                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                    InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb_propeptide;
                                                                                                                                                                                                                                                                                                                                                                          ZFIN;
                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDF8 OR MSTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Growth/differentiation
                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                   Growth
                                                                                                                                                                                                                                                                                             SMART; SM00204; TGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359
                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                          ProDom;
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                           266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
 61
                                                                                           Local
                                                     ,_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY). SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUSCLE GROWTH
  VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS
                           DSGLDCDENSSESRCCRYPLTVDFEDFGWDWIIAPKRYKANYCSGECDYMYLQKYPHTHL
                                                   DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHQANPRGSAGECCTETKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLGLDCDEHSSESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHL 358
                                                                                                                                                                                                                                                                                                                                                                          ZDB-GENE-990415-165;
                                                                                                                                                                                                                                                                                                                                                                                         P18075;
                                                                                                                                                                                                                                                                                                                                                                                                    AF019626;
                                                                                                                                                                                                                                                                  factor;
                                                                                           Similarity
                                                                                                                                                                                                                                                                                                          PD000357;
                                                                                                                                                                                                                                                                               PS00250;
                                                                                                                                  374 AA;
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                         1BMP
                                                                                                                                                                                                                                                                  Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                      AAB86693.1; ~.
                                                                                                                                                                                                                                                                             TGF_BETA_1;
                                                                                                                                                                                                                                                                                                        TGFb;
                                                                                          88.7%;
                                                                                                                                  42060 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor 8 precursor (GDF-8) (Myostatin)
                                                                                                                                                                                                                                                                Glycoprotein; Signal.
                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                          gdf8.
                                                                                          Score 559; DB 1;
Pred. No. 4.5e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Craniata;
Teleostei;
                                                                                                                                              N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                    BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                           POTENTIAL.
GROWTH/DIFFERENTIATION FACTOR
                                                                                                                                                                         INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                   6302BC6C86562576 CRC64;
                                                                                Mismatches
                                                                                                                                                                                                     SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                       Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cypriniformes;
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Best Local
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RAT
GDFB RAT
Q9Z217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Expression of growth/differentiation factor 11, a new member Mech. Dev. 80:185-189(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Dental pulp;
MEDLINE=99173787; PubMed=10072786;
Makashima M., Toyono T., Akamine A., J
"Expression of growth/differentiation
MMD/MCEbeta manageria."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, L
16-OCT-2001 (Rel. 40, L
Growth/differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDF11 OR BMP11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P18075; 1BMP.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                            NON TER
                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 VNKASPRGTAGPCCTPTKMSPINMLYFNGKEQIIYGKIPSMVVDRCGCS 374
                           303
                                                                                                                              243
                                                                         61
                                                                                                                                                         1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN (BY SIMILARITY). SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted (Probable). SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT. PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Fragment
                                                      VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVV 103
                                                                                                                           NLGLDCDEHSSESRCCRYPLTVDFEASGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHL 302
                        VQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPGMVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00019; TGF-beta; 1.
PF00688; TGFb propeptide;
m; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF092733;
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                                                                                                                                                                                                                                                   Similarity
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
(Rel. 40, Last annotation (Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                             345 AA;
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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>345
159
316
315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                 83.5%;
                                                                                                                                                                                                                                                                                                                             39094 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein.
                                                                                                                                                                                                                                                 Score 526; DB 1
Pred. No. 2e-51;
                                                                                                                                                                                                                                                                                                                                                                            POLY-GLY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GROWTH/DIFFERENTIATION FACTOR 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                             81D5B93FED6B0443 CRC64;
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345
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                                                                                                                                                                                                                                                                         DB 1; Length 345
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  RESULT 14
IHBB_MOUSE
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Growth f
NON TER
PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENT INTERIORS INTERIORS INHIBIT AND ACTIVATE,
-1- FUNCTION: INHIBING AND ACTIVINS INHIBIT AND ACTIVATE,
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
FUNCTIONS SUCH AS HYPOTHALANIC AND PITUITARY HORMONE SECRETION,
GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
ENERYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
ACTIVINS.
-1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN A IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-B.
ACTIVIN AS IS A HOMODIMER OF BETA-B.
ACTIVIN AS IS A DIMER OF BETA-B.
ACTIVIN BIS A DIMER OF BETA-B.
BETA-B.
ACTIVIN BIS A DIMER OF BETA-B.
BETA-B.
ACTIVIN BIS A DIMER OF BETA-B.
BETA
                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Activin disrupts epithelial branching morphogenesis in developing glandular organs of the mouse."; Mech. Dev. 50:229-245(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                     InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PR00019; TGF-beta; 1.
Pfam; PF00688; TGFb propeptide;
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                           EMBL; X83376; CAA58290.1; -. EMBL; X69620; CAA49326.1; -. PIR; S31441; S31441.
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"Activins are expressed in preimplantation mouse embryos a and EC cells and are regulated on their differentiation.";
Development 117:711-723(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CBA X NMR1; TISSUE=Testis;
MEDLINE=95344997; PubMed=7619733;
Ritvos O., Tuuri T., Eramaa M., Sainio K., Hilden K., Saxen L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-234 FROM N.A
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                                                 PROSITE; PS00250; tor_____Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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  POTENTIAL.
INHIBIN BETA B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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AC P2709
DT 01-NC
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OC Galthu
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-ROV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Inhibin beta B chain precursor (Activin beta-B chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=White leghorn; TISSUE-Ovary;
Hecht D.J., Davis A.J., Ryan I.M., Johnson P.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IHBB CHICK
P27093; 073796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klinger H., Halaschek-Wiener J., Wohlrab B.K., Kuchler K., Wohlrab F.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 PHTAVVNQYRMRGLNPGPVNSCCIPTKLSSMSMLYFDDBYNIVKRDVPNMIVEECGCA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141
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Pred. No. 7.5e-21;
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Best Local
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InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00648; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PRODOm; PD000357; TGFb; 1.
                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                       SEQUENCE
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EMBL; AF055478; AAC14187.1; -.
                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M61166; AAA48568.1; -. EMBL; M57408; AAA03079.1; -. HSSP; P18075; 1BMP.
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                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                     Growth factor;
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PROSITE; PS00250; TGF_BETA_1; 1
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334 FHTAVVNOYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 391
                                                 277 GLECDGRT--NLCCRQQFYIDFRLIGWNDWIIAPSGYYGNYCEGSCP-AYLAGVPGSASS 333
                      57 -HTHLVHQANPR----GSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                   3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP-----
                                                                                                                 Similarity
                                                                                                     Conservative
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060017BF33F7AF6C CRC64;
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                                                                                                                              DB 1;
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2: pir2:*
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4: pir4:*
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PW0042
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## ALIGNMENTS

RESULT 1

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: RMBL:K83376; NID:g603571; PIDN:CAA58290.1; PID:g603572
A;Cross-references: RMBL:K83376; NID:g603571; PIDN:CAA58290.1; PID:g603572
R;Albano, R.M.; Groome, N.; Smith, J.C.
Development 111, 711-723, 1993
A;Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cells
A;Reference number: 148243; MUID:93321614; PMID:8330535
A;Accession: 148266
                                                                                                                                                                                                                                                                                                                                        inhibin beta-B chain - mouse (fragment)
N;Alternate names: activin bB chain
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence revision 01-Aug-1997 #text_change 16-Jul-1999
C;Accession: I48235; I48266; S31441
R;Ritvos, 0.; Tuuri, 7.; Eramaa, M.; Sainio, K.; Hilden, K.; Saxen, L.; Gilbert, S.F.
Mech. Dev. 50, 229-245, 1995
Mech. Dev. 50, 229-245, 1995
A;Title: Activin disrupts epithelial branching morphogenesis in developing glandular org
A;Reference number: 148235; MUID:95344997; PMID:7619733
A;Accession: I48235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Dohrmann, C.E.; Hemmati-Brivanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Melton, Dev. Biol. 157, 474-483, 1993
A;Title: Expression of activin mRNA during early development in Xenopus laevis.
A;Reference number: 151199; WUID:93273083; PMID:8500654
A;Accession: 151199
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C;Species: Xenopus laevis (African clawed frog)
C;Bate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: I51199
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A; Residues: 1-370 < DOH >
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 GLECDGHT--NLCCROOFYIDERLIGWNDWIIAPAGYYGNYCEGSCP-AYLAGVPGSASS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 -HTHLUHQANPR----GSAGPCCTFTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
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C;Date: 03-Apr-1992 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999 (;Accession: B41398, I55288; C40905 R;Feng, E.M.; Li, Y.P.; Chen, C.L.C. Mol. Endocrinol. 3, 1914-1925, 1989 A;Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subunit ge A;Reference number: A41398; MUID:90190649; PMID:2628729 A;Accession: B41398
activin b%ta B-2 chain - goldfish (fragment)
N;Alternate names: gact 11
C;Species: Carassius auxatus (goldfish)
C;Date: 31_Dec_1993 #sequence_revision 31-Dec_1993 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:S72477; NID:9619268
R;Esch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Ueno, N. Mol. Endocrinol. 1, 388-396, 1987
Mol. Endocrinol. 1, 388-396, 1987
A;Title: Complementary deoxyribonucleic acid (CDNA) Cloning and DNA sequence analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 134,'D',136-255 <ALB>
A;Cross-references: EMBL:X69620, NID:g50147; PIDN:CAA49326.1, PID:g50148
C;Superfamily: inhibin
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A; Residues: 133-411 <ESC>
C; Superfamily: inhibin
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A; Residues: 1-7 < RES>
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                                                                                                                                                                                                                                                                   354 FHTAVVNOYRMRĞLNPĞPVNSCCIPTKLSSMSMLYFDDEYNIVKRDVPNMIVEECĞCA 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP----- 56
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                                                                                                                                                                                                                                                                                                                                                                                              GLECDGRT--SLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCP-AYLAGVPGSASS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-174 <FEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n 39.8%;
Similarity 44.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 251; DB 2;
Pred. No. 2.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 411;
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A; Molecule type: mRNA
A; Residues: 1-349 < MAS>
A; Residues: 1-340 < MAS>
A; Cross-references: GB: X03267; NID: g2005; PIDN: CAA27021.1; PID: g2006
C; Comment: The source of this protein is ovarian followlar fluid.
C; Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptid ifferent forms of inhibin have been isolated (A and B) that differ in the amino-terminal C; Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of follit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibin beta-B chain precursor - pig (fragment)
C;Species: Sus acrofa domestica (domestic pig)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000
C;Accession: A01394
C;Accession: A01394
R;Mason, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemin, R.;
Nature 318, 659-663, 1985
R;Mason, A.J.; Berkemeier, L.M.; Schmelzer, C.H.; Schwall, R.H. Mol. Endocrinol. 3, 1352-1358, 1989
Mol. Endocrinol. 3, 1352-1358, 1989
A;Title: Activin B: precursor sequences, genomic structure and in vitro activities. A;Reference number: A40150; MUID:90114200; PMID:2575216
A;Accession: A40150
                                                                                                                                                                                                                                                           N;Alternate names: activin AB chain B C;Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A01394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor A, Reference number: A93371; MUID:86092207; PMID:2417121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
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A; Residues: 1-115 < GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: PN0506
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Biochem. Biophys. Res. Commun. 193, 711-717, 1993
A;Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural con
A;Reference number: PNO504; MUID:93290666; PMID:8512569
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
                                                                                                                                                                                                                                                                                                                                         nhibin beta-B chain precursor - human
                                                                                                                                                                                      Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 01-Dec-2000; Date: 10-Sep-1999 #cxt_change 01-Dec-2000; Accession: A40150; C24240; A40156; S10751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 FHTAVVNQYRMRGINPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVENMIVEECGCA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 -HTHLVHQANPR----GSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 FHTAVVNOYRMRCMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGC 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP----- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GLECD-GTNGGLCCRQQFYIDFRLIGWNDWIIAPAGYYGNYCEGSCP-AFLAGVPGSASS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP---- 56
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sin: propeptide (fragment) #status predicted <PRO>_
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43.6%; Pred. No. 1.8e-19;
tive 13; Mismatches 40
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                                                                                                                                                            Schmelzer, C.H.; Schwall, R.H.
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Pred. No. 1.1e-18
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A; Molecule type: DNA A; Residues: 1-407 < MAS>

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A;Molecule type: mRNA,
A;Molecule type: mRNA,
A;Residues: 55-407 <MA2>
A;Residues: 55-407 <MA2>
A;Residues: 55-407 <MA2>
A;Croos-references: GB:M13437; NID:g186416; PIDN:AAA59169.1; PID:g186417
A;Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.
Mol. Endocrinol. 3, 939-948, 1189
Mol. Endocrinol. 3, 939-948, 1189
A;Tille: Characterization and regulation of testicular inhibin beta-subunit mRNA.
A;Tille: Characterization and regulation of testicular inhibin beta-subunit mRNA.
A;Reference number: A40156; MUID:89295443; PMID:2739657
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A;Reference number: A90123; MUID:86186863; PMID:3754442 A;Accession: C24248
                                                                                                                                                                                                                                                                                                                                                   R;Thompson, D.A.; Cronin, C.N.; Martin, F.
Eur. J. Biochem. 226, 751-764, 1994
A;Title: Genomic Cloning and sequence analyses of the bovine alpha-, beta(A)- and beta
                                                                                                                                                                                                                                                                                                                                                                                                                                              betaB inhibin precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C;Accession: S50899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone F;1-20/Domain: signal sequence #status predicted <SIG>F;1-29/Domain: propeptide #status predicted <PRO>F;293/Product: inhibin beta-B chain #status predicted <WAT>F;99/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Residues: 293-294, 'GX', 297-302, 'XX', 305-307 <SCH>
C;Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respection beta-A and beta-B, respectively.
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R;Schmelzer, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois, N. Biochim. Biophys. Acta 1039, 135-141, 1990
A;Title: Purification and characterization of recombinant human activin B.
A;Reference number: S10751; MUID:90304183; PMID:2364091
                                                                                A; Introns: 151/1
C; Superfamily: inhibin
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A; Residues: 22-46, 'A',
                                                                                                                                                                    A; Cross-references: EMBL: U16240
                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-408 <THO>
                                                                                                                                                                                                                                                                         y DNase I footprinting. A; Reference number: S50897; MUID:95112839; PMID:7813465 A; Accession: S50899
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C, Superfamily: inhibin
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   Query Match
Best Local Similarity
                                                                                                                                           Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 FHTAVVNÓYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVÞNMIVEECGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 GLECDGRT--NLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCP-AYLAGVPGSASS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 -HTHLVHQANPR----GSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.9%; Score 245; DB 1; Length 407; 41.5%; Pred. No. 1.2e-18;
   38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
Score 245; DB 2;
Pred. No. 1.2e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                         Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-115 <GE
C; Superfamily: inhibi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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NyAlternate names; gact 2
C;Species: Carassius auratus (goldfish)
C;Species: Decc-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PN0505
R;Ge, W; Gallin, W.J.; Strobeck, C; Peter, R.E.
Biochem. Biophys. Res. Commun. 193, 711-717, 1993
B;Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural con A;Reference number: PN0504, MUID:93290666; PMID:8512569
B;Accession: PN0505
B;Accession: PN0505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activin beta B - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: I50103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: Zactuera.
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activin beta B-1 chain - goldfish (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 FHTAVVNQYRMRGMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 GLECDGNN-GGLCCRQQFYIDFRLIGWNDWIIAPAGYYGNYCEGSCP-AYMAGVPGSASS 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 FHTAVVNÓYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 -HTHLVHQANPR----GSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                               57 -HTHLVHQANPR----GSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 -HTHLVHQANPR----GSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
59 FHTAVVNOYRMRGISPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGC 115
                                                                                                                               3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP----- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP---- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP---- 56
                                                                                     GLECD-GINGGLCCROOFYIDFRLIGHNDWITAPAGYYGNYCEGSCP-AYMAGVPGSASS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLECDGRT--NLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCP-AYLAGVPGSASS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
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                                                                                                                                                                                                38.5%; Score 242.5; DB 2; Length 115; 41.9%; Pred. No. 6.3e-19;
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Pred. No. 1.4
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                                                                                                                                                                                40;
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vgr protein - rat (fragment)
C./Species: Rattus norvegicus (Norway rat)
C./Species: Rattus norvegicus (Norway rat)
C./Species: Rattus norvegicus (Norway rat)
C./Accession: S37618
R./Sauermann, U./Meyermann, R./Schluesener, H.J.
J. Neurosci. Res. 33, 142-147, 1992
J. Patrosci. Res. 33, 142-147, 1992
A./Fitle: Cloning of a novel TGF-beta related cytokine, the A/Reference number: S37618; MUID:93085758; PMID:1453478
A/Accession: S37618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:BMP6
A;Gross references: GDB:127596; OMIM:112266
A;Map position: 6pter-6qter
C;Superfamily: inhibin
C;Superfamily: inhibin
C;Superfamily: inhibin
C;Superfamily: inhibin
C;Superfamily: bone morphogenet #status predicted <SIG>
F;1-23/Domain: signal sequence #status predicted <PRO>
F;44-374/Domain: propeptide #status predicted cPRO>
F;47-5-513/Product: bone morphogenetic protein 6 #status predicted <MAT>
F;241,269,386,404,454/Binding site: carbobydrate (Asn) (covalent) #statu
Vg-1-related protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
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A;Title: Identification of transforming growth factor beta family members present in bon A;Reference number: A39263; MUID:91088608; PMID:2263636
A;Accession: B39263
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A,NOte: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 88-Ser
C;Superfamily: inhibin
                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone morphogenetic protein 6 precursor - human C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :Molecule type: mRNA
:Residues: 1-513 <CEL>
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Date: 18-Feb-1994 #sequence_revision 26-May-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                               462 QTLVHLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGC 512
                                                                                                                                                                                                                                                                                                                                                                                                                                             402 DYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIV 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 OTLVHLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGC 206
                                                                                                                                                                                                                                                                                                                                                                  60 -- LVHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGC 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 DCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYPHTH---- 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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activin - fruit fly (Drosophila sp.) (fragment)
C;Species: Drosophila sp.
C;Species: Drosophila sp.
C;Date: 18-70un-1998 #sequence_revision 10-Jul-1998 #text_change 17-Nov-2000
C;Accession: PW0042
R;Kutty, G.; Kutty, R.K.; Samuel, W.; Duncan, T.; Jaworski, C.; Wiggert, B.
Biochem. Biophys: Res. Commun. 246, 644-649, 1998
Biochem. Biophys: Res. Commun. 246, 644-649, 1998
A;Tille: Identification of a new member of transforming growth factor-beta superfamily i
A;Reference number: PW0042; MUID:98289585; PMID:9618266
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R;Gitelman, S.E.; Kobrin, M.S.; Ye, J.Q.; Lopez, A.R.; Lee, A.; Derynck, R.
J. Cell Biol. 126, 1595-1609, 1994
A;Title: Recombinant vgr-1/BMP-6-expressing tumors induce fibrosis and endochondral bone A;Reference number: A54798; MUID:94375533; PMID:8089189
A;Accession: A54798
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C; Superfamily: inhibin
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A; Residues: 1-510 <GIT>
A; Residues: 1-510 <GIT>
A; Cross-references: EMBL:X80992; NID:g530729; PIDN:CAA56917.1; PID:g530730
A; Cross-references: EMBL:X80992; NID:g530729; PIDN:CAA56917.1; PID:g530730
A; Chen, E.Y.; Hogan, B.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1999
A; Title: Vgr-1, a mammalian gene related to Xenopus Vg-1, is a member of the transformin A; Reference number: A33925; MUID:89282810; PMID:2734307
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PW0042
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A;Residues: 'M',74,'K',76-85,'P',87-510 <LYO>
A;Cross-references: GB:J04566; NID:g202352; PIDN:AAA40548.1; PID:g202353
C;Superfamily: inhibin
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A; Residues: 1-373 < KUT>
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Start codon: GGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 DYNGSELKTACKKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIV 458
320 AHFIEEYRKMGLMNGMRPCCAPIKFSSMSLIYYGDDG-IIKRDLPKMVVDECGC 372
                                                                                                                                     262 VDCG-GALNGQCCKESFYVSFKÄLGWDDWIIAPRGYFANYCRGDCTGSFRTPDTFQTF-H
                                                                58 THLVHQANPRG---SAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGC 108
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47; Conservative
                                                                                                                                                                                                                                                                  34.9%; Score 220; DB 2; Length 373; Similarity 39.5%; Pred, No. 5.5e-16; Similarity 39.5%; Pred, No. 5.5e-16; Indels 45; Conservative 17; Mismatches 40; Indels
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42.3%; Pred. No. 5.6e-17;
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transforming growth factor beta homolog - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000 C;Accession: T25451

RESULT 14 T25451

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bone morphogenetic protein homolog GDF6 precursor - mouse (fragment) N;Alternate names: growth and differentiation factor 6 C;Specias: Mus musculus (house mouse) C;Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000 C;Accession: S43295
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Submitted to the EMBL Data Library, December 1996

A; Description: The sequence of C. elegans cosmid B0412.

A; Reference number: Z20037

A; Accession: T25451
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A;Introns: 43/3; 123/3; 184/2; 288/3
C;Superfamily: inhibin
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A;Residues: 1.350 <BEN>
A;Cross-veferences: EMBL:U80953; PIDN:AAB52554.1; GSPDB:GN00021
A;Experimental source: Strain Bristol N2; clone B0412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: ddf6
G;Superfamily: inhibin
F;1-5/Domain: polybasic protease recognition site #status predicted <PPR>
F;6-125/Product: bone morphogenetic protein homolog GDP6 (fragment) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-125 <STO>
A;Cross-references: EMBL:U08338; NID:g488463; PIDN:AAA18779.1; PID:g488464
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A;Title: Limb alterations in brachypodism mice due to mutations in a new member of the A;Reference number: S43294; MUID:94195427; PMID:8145850
A;Accession: S43295
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Search completed: January 31, 2003, 18:18:59 Job time : 15 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 HQA----NPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
                                                                                                                           76 LMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGC 124
                                                                                                                                                                                 60 LVHQANPRGSAGPCCTPTKMSPINMLYPNGEGQIIYGKIPAMVVDRCGC 108
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                                                                                                                                                                                                                                                                                     9 HSTES--RCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKY-PHTH----- 59
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nilarity 34.8%; Pred. No. 6.6e-16;
Conservative 20; Mismatches 43; Indels 10; Gaps
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Maximum Match 100%
Listing first 45 su
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Maximum DB seq length: 2000000000
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A29619
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          bone morphogenetic activin beta C - m activin beta C pre bone morphogenetic
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inhibin beta-B cha
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A;Title: Expression of activin mRNA during early development in Xenopus laevis. A;Reference number: I51199, MUID:93273083; PMID:8500654
A;Accession: I51199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activin beta B subunit - African clawed frog
C;Species: Xenopus Laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: I51199
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A; Residues: 1-370 < DOH >
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Hemmati-Brivanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Melton,

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-234 <RES>
A;Residues: 1-234 <RES>
A;Cross-references: EMBL:X83376; NID:g603571; PIDN:CAA58290.1; PID:g603572
R;Albano, R.M.; Groome, N.; Smith, J.C.
Development 117, 711-723, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibin beta-B chain - mouse (fragment)
N;Alternate names: activin bB chain
C;Species: Mus muscullus (house mouse)
C;Date: 02-Jul-1996 #sequence revision 01-Aug-1997 #text_change 16-Jul-1999
C;Accession: I4825; I48266; S31441
C;Accession: 0, Tuuri, T.; Eramaa, M.; Sainio, K.; Hilden, K.; Saxen, L.; Gilbert, S.F.
R;Ritvos, O, Tuuri, T.; Eramaa, M.; Sainio, K.; Hilden, K.; Saxen, L.; Gilbert, S.F.
Mech, Dev. 50, 229-245, 1995
A;Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cells A;Reference number: 148243; MUID:93321614; PMID:8330535 A;Accession: I48266 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                           A,Title: Activin disrupts epithelial branching morphogenesis in developing glandular org
A,Reference number: I48235; MUID:95344997; PMID:7619733
A,Accession: I48235
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C;Superfamily: inhibin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 GLECDGHT--NLCCROOFYIDFRLIGWNDWIIAPAGYYGNYCEGSCP-AYLAGVPGSASS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 -HTHLVHQANPR----GSAGPCCTPTKMSPINMLYFNGKEQIIXGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.4%; Score 254; DB 2
42.4%; Pred. No. 8e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
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A;Molecule type: mRNA
A;Residues: 114','D',136-255 <ALB>
A;Cross-references: EMBL:X69620; NID:g50147; PIDN:CAA49326.1; PID:g50148
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                               В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Two messenger ribonucleic acids encoding the common beta B-chain of inhibin and A;Reference number: I53288; MUID:94307180; PMID:8033818
A;Accession: I53288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Feng, Z.M.; Li, Y.P.; Chen, C.L.C.
Mol. Endocrinol. 3, 1914-1925, 1989
A;Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subunit ge
A;Reference number: A41398; MUID:90190649; PMID:2628729
A;Accession: B41398
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N;Alternate names: inhibin/Activin beta B-chain
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Apr-1992 #sequence revision 01-Aug-1997 #text_change 16-Jul-1999
C;Accession: B41398; I53288; C40905
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activin beta B-2 chain - goldfish (fragment)
N,Alternate names: gact 11
C;Species: Carassius auratus (goldfish)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PN@506
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C;Superfamily: inhibin
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A; Residues: 133-411 < ESC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:S72477; NID:9619268
R;Bsoch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Ueno, Mol: Endocrinol. 1, 388-396, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Dykema, J.C.; Mayo, K.E.
Endocrinology 135, 702-711, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-174 < FEN >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-7 < RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 GLECDGRT--SLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCP-AYLAGVPGSASS 197
                                                                                                                                                                                                                                                                                           354 FHTAVVNQYRMRGLNPGPVNSCCIPTKLSSMSMLYFDDEYNIVKRDVPNMIVEECGCA 411
                                                                                                                                                                                                                                                                                                                                                                                                                   297 GLECDGRT--SLCCRQQFFIDFRLIGWNDWIIAFTGYYGNYCEGSCP-AYLAGVFGSASS 353
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                                                                                                                                                                                                                                                                                                                                                 57 -HTHLVHQANPRG-SAGP---CCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GLDCDEHSTESRCCRYPLTVDFEAPGW-DWIIAPKRYKANYCSGECEFVFLQKYP----- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.4%; Score 248; DB 2
43.2%; Pred. No. 4e-19;
ative 17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 411;
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A; Accession: A01394

A, Molecule type: mRNA

A; Residues: 1-349 <-MAS>
A; Cross-references: GB:X0267; NID:g2005; PIDN:CAA27021.1; PID:g2006

C; Comment: The source of this protein is ovarian follicular fluid.

C; Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptid ifferent forms of inhibin have been isolated (A and B) that differ in the amino-terminal c; Comment: Ilhibin is secreted by ovaries or testes and inhibits the secretion of follit c; Superfamily: inhibin
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Biochem. Biophys. Res. Commun. 193, 711-717, 193
A;Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural con
A;Reference number: PN0504; MUID:93290666; PMID:8512569
A;Accession: PN0506
A;Molecule type: DNA
A;Residues: 1-115 <GEM>
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: contraceptive; follitropin inhibitor; glycoprotein; gonad F;1-334/Domain: propeptide (fragment) #status predicted <PRO>F;1-335-349/Product: Inhibin beta-B chain #status predicted <NAT>F;35/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibin beta-B chain precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000
C;Accession: A01394
R;Mason, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Gu:
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RESULT 6
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                                                                                                292 FHTAVVNOYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 349
                                                                                                                                                                                                                                         235 GLECDGRT--NLCCROOFFIDFRLIGWSDWIIAFTGYYGNYCEGSCP-AYLAGVPGSASS 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 FHTAVVNOYRMRGMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 -HTHLVHQANPR----GSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGC 108
                                                                                                                                                                         57 -HTHLVHQANPR----GSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                              h 38.5%; Score 242; DB 1; Similarity 40.7%; Pred. No. 1.5e-18; 48; Conservative 18; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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42.7%; Pred. No. 2.6e-19;
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C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 01-Dec-2000
C;Accession: A40150; C24248; Ā40156; S10751
R;Mason, A.J.; Berkemeier, L.M.; Schmelzer, C.H.; Schwall, R.H.
Mol. Endocrinol. 3, 1352-1358, 1989
A;Title: Activin B: precursor sequences, genomic structure and in vitro activities.
A;Reference number: A40150; MUID:90114200; PMID:2575216
A;Accession: A40150

A; Molecule type: DNA A; Residues: 1-407 < MAS> inhibin beta-B chain precursor - human N;Alternate names: activin AB chain B

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R;Thompson, D.A.; Cronin, C.N.; Martin, F.
Bur. J. Biochem. 226, 751-764, 1994
A;Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)-
y DNase I footprinting.
A;Reference number: S50897; MUID:95112839; PMID:7813465
A;Accession: S50899
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(;Superfamily: inhibin
C;Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-292/Domain: propeptide #status predicted <PRO>
F;21-292/Domain: beta-B chain #status predicted <ART>
F;293/Product: inhibin beta-B chain #status predicted <ART>
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R;Schmelzer, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.;
Biochim. Biophys. Acta 1039, 135-141, 1990
A;Title: Purification and characterization of recombinant human activin B.
A;Reference number: S10751; MUID:90304183; PMID:2364091
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Mol. Endocrinol. 3, 939-948, 1989

A;Title: Characterization and regulation of testicular inhibin beta-subunit mRNA.

A;Reference number: A40156; MUID:89295443; PMID:2739657

A;Accession: A40156
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A; Rolecule type: mRNA
A; Residues: 55-407 < MA2>
A; Cross-references: GB:M13437; NID:g186416; PIDN:AAA59169.1; PID:g186417
A; Cross-references: GB:M13437; Chen, C.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M31668; GB:M31669; NID:g186419; PIDN:AAA59451.1; PID:g386827 R;Mason, A.J.; Niall, H.D.; Seeburg, P.H. Biochem. Biophys. Res. Commun. 135, 957-964, 1986 A;Title: Structure of two human ovarian inhibins. A;Reference number: A90123; MUID:86186863; PMID:3754442 A;Accession: C24248
                                                                             A; Introns: 151/C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C;Accession: S50899
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A;Residues: 293-294,'GX',297-302,'XX',305-307 <SCH>
C;Comment: Activins A and B are homodimers of inhibin
bin beta-A and beta-B, respectively.
                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-408 < THO>
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A; Residues: 22-46, 'A', 48-407 < FEN>
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                                                                                                                                        Genetics:
                                Query Match
                                                                                                                                                                      Cross-references: EMBL:U16240
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Best Local
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     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -HTHLVHQANDR-----GSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLECDGRT--NLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCP-AYLAGVPGSASS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 407
                                                                                                                151/1
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  38.5%;
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Pred. No. 1.8e-18;
Score 242; DB 2;
Pred. No. 1.8e-18;
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                          Length 408;
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A; Molecule type: DNA
A; Residues: 1-115 <GEW>
C; Superfamily: inhibin
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PN0505
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Genes Dev. 8, 1448-1462, 1994
A;Title: Disruption of mesoderm and axis formation in fish
A;Reference number: I50103; MUID:95011555; PMID:7926744
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C;Species: Brachydanio rerio (zebra fish)
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A; Residues: 1-393 <WIT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 -HTHLVHQANPR----GSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
59 FHTAVVNQYRMRGISPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGC 115
                                                                                                                                                                  FOCAT
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                                                                                                            3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP----- 56
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                                    -HTHLVHQANPR----GSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGC 108
                                                                        GLECD-GTNGGLCCRQQFYIDFRLIGWNDWIIAPAGYYGNYCEGSCP-AYMAGVPGSASS 58
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                                                                                                                                                                38.1%; Score 239.5; DB 2
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Pred. No. 1.9e-18;
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                                                                                                                                                                                    DB 2;
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RESULT 10

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RESULT 11
BMHU6
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C;Date: 18-Feb-1994 #sequence_revision 26-May-1995 #text_change 16-Jul-1999
C;Date: 18-Feb-1994 #sequence_revision 26-May-1995 #text_change 16-Jul-1999
C;Accession: S37618
R;Sauermann, U; Meyermann, R.; Schluesener, H.J.
J. Neurosci. Res. 33, 142-147, 1992
A;Title: Cloning of a novel TGF-beta related cytokine, the vgr, from rat brank, Reference number: S37618; MUID:93085758; PMID:1453478
Vg-1-related protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1-23/Domain: signal sequence #status predicted <SIG>F;24-374/Domain: propeptide #status predicted <PRO>F;34-374/Domain: propeptide #status predicted <PRO>F;375-513/Product: bone morphogenetic protein 6 #status predicted <MAT>F;241,269,386,404,454/Binding site: carbohydrate (Asn) (covalent) #statu
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A;Map position: 6pter-6qter
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozn Proc. Natl. Acad. Sci. U.S.A. 87, 8843-9847, 1990
A;Title: Identification of transforming growth factor beta family members present in bor A;Reference number: A39263; MUID:91088608; PMID:2263636
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A;Molecule type: mRNA
A;Residues: 1-207 <SAU>
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A; Residues: 1-513 < CEL>
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                                                                                                                                RESULT 12 .
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Best Local :
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Best Local :
                                                                                                                                                                                                                                                                                                                                 402 DYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIV 461
                                                                                                                                                                                                                   462
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                                                                                                                                                                                                                                                                       60 -- LVHQANPRGSAGECCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Loca1
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                                                                                                                                                                                                                                                                                                                                                                                      5 DCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYPHTH---- 59
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                                                                                                                                                                                                                QTLVHLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Mismatches
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Pred. No. 2.4e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
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V91 embryonic growth factor - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 21-Jul-2000 C;Accession: A29619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X80992; NID:g530729; PIDN:CAA56917.1; PID:g530730 R;Lyons, K.; Graycar, J.L.; Lee, A.; Hashmi, S.; Lindquist, P.B.; Chen, E.Y.; Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989 A;Title: Vgr-1, a mammalian gene related to Xenopus Vg-1, is a member of the tA;Reference number: A33925; MUID:89282810; PMID:2734307 A;Accession: A33925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: A54798; A33925; S47442
R;Gitelman, S.E.; Kobrin, M.S.; Ye, J.Q.; Lopez, A.R.; Lee, A.; Derynck, R.
J. Cell Biol. 126, 1595-1609, 1994
A;Title: Recombinant vgr-1/BMP-6-expressing tumors induce fibrosis and endochondral bone A;Reference number: A54798; MUID:94375533; PMID:8089189
A;Accession: A54798
                                                                                                                                                                                                                                                                                                                             A;Regidues: 1-360 <WEE>
A;Cross-references: GB:M18055; NID:g214179; PIDN:AAA49727.1; PID:g214180
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                A, Title: A maternal mRNA localized to the vegetal hemisphere in A; Reference number: A29619; MUID:88052889; PMID:3479264
A; Accession: A29619
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A;Residues: 'M',74,'K',76-85,'P',87-510 <LYO>
A;Cross_references: GB:J04566; NID:g202352; PIDN:AAA40548.1; PID:g202353
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A; Residues: 1-510 < GIT>
                                                                                                                                                                                                                                                                                                       C; Keywords: growth factor
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313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 DYNGSELKTACKKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIV 458
                                                                                                     259 CKKRHLYVEFKDVGWQNWVIAPQGYMANYCYGEC-----PYPLTEILNGSNHAILQTLV 312
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                                              HQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGC 108
                                                                                                                                                 CCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYPHTH-------
HSIEPEDIPLPCCVPTKMSPISMLFYDNNDNVVLRHYENMAVDECGC 359
                                                                                                                                                                                                       43;
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                                                                                                                                                                                                                             34.9%;
Similarity 40.2%;
                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                             Score 219.5; DB 2
Pred. No. 4.2e-16;
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Pred. No. 3.9e-17;
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                                                                                                                                                                                                                                                         DB 2;
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bone morphogenetic protein homolog GDP6 precursor - mouse (fragment)
N;Alternate names: growth and differentiation factor 6
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence\_revision 07-Feb-1997 #text\_change 26-May-2000

E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, 68, 639-643, 1994

S.J.

R;Storm,

368,

C; Accession: S43295

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cartilage-derived morphogenetic protein 2 precursor - bovine (fragment) (;Species: Bos primigenius taurus (cattle) (;Decies: Bos primigenius taurus (cattle) (;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000 (;Accession: B55452 R;Chang, B.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak J. Biol. Chem. 269, 28227-28234, 1994 A;Title: Cartilage-derived morphogenetic proteins. New members of the transforming growt A;Reference number: A55452; MUID:95050604; PMID:7961761 A;Accession: B55452
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A;Molecule type: mRNA
A;Molecule type: cCHA>
A;Residues: 1-436 - CCHA>
A;Cross_references: GB:U13661; NID:g632489; PIDN:AAA61416.1; PID:g632490
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Search completed: January 31, 2003, 18:18:58 Job time : 14 secs
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34.7%; Score 218.5; DB 2; Length 436;
Best Local Similarity 38.5%; Pred. No. 6.6e-16;
Matches 42; Conservative 20; Mismatches 38; Indels 9; Gaps
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Superfamily: inhibin
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P30886 P34820 P18075 P43029 P23359 P43026 P43026 P55103 P48970 P27092

6 xenopus lae
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homo sapien
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gallus gall
caenorhabdi

mus musculu

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                      242
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Copyright (c) 1993 - 2003 Compugen Ltd.
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DVR1 BRARE
IHBB CHICK
THBB PIG
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BMP6 MOUSE
IHBA HORSE
DVR1 XENLA
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GDF8_HUMAN
GDF8_MELGA
GDF8_PIG
GDF8_NOUSE
GDF8_PAPHA
GDF8_PAPHA
GDF8_BOVIN
GDF8_BOVIN
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GDF8_RAT
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GDF8_RAT
GDF8_RAT
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IHBA_RAT
IHBA_BOVIN
IHBA_SHEEP
IHBA_HUMAN
IHBC_MOUSE
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GDF6_BOVIN
IHBA_MOUSE
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                                                                             8 mus musculu
6 bos taurus
8 mus musculu
0 mus scrofa
1 rattus norv
5 bos taurus
2 ovis aries
6 homo sapien
4 mus musculu
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2 rattus norv
8 papio hamad
0 ovis aries
6 bos taurus
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mus musculu
equus cabal
xenopus lae
mus musculu
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brachydanio
gallus gall
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homo sapien
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042220;
042220;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8) (Myostatin)
GDF8 OR MSTN.
GB11US (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAINSWhite leghorn; TISSUB-Skeletal muscle;
MEDLINE-98024153; PubMed-9356471;
MCPHORITON A.C., Lee S.-J.;
MCPHORITON A.C., Lee S.-J.;
POOLDIE muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S. A. 94:12457-12461(1997).
-(- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUSCLE GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
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DAF7 CAEEL
GDF3 MOUSE
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BMP8 HUMAN
BMP7 HUMAN
BMP7 HUMAN
GDP7 MOUSE
BMP7 MOUSE
GDP5 MOUSE
GDP5 HUMAN
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a collaboration

Result No.

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Matches
          DISULFID.
                                                                  Growth factor; (SIGNAL 1
PROPEP 24
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15-UUL-1999 (Rel. 38, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                            ProDom; PDUVVVJ.,
SMART; SM00204; TGFB; 1.
SMART; SM00204; TGF_BETA 1;
                                                                                                                                                InterPro, IPR001111; TGFb N.
Pfam; PP00019; TGF-beta; I.
Pfam; PF00688; TGFb propeptide; 1.
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                        EMBL; AF104922; AA(
HSSP; P18075; 1BMP
                                                                                                                                                                                                                                                                          EMBL; AF1019627; AAB86694.1; -. EMBL; AF104922; AAC96327.1; -.
                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arver S., Bhasin S.;
"Organization of the human myostatin gene and expression in healthy moranization of the human myostatin gene and expression in healthy men and HUV-infected men with muscle wasting.";
Proc. Natl. Acad. Sci. U.S.A. 95:14938-14943(1998).
-I- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99061972; PubMed=9843994;
Gonzalez-Cadavid N.F., Taylor W.E., Yarasheski K., Sinha-Hikim I.,
Ma.K., Ezzat S., Shen R., Lalani R., Asa S., Mamita M., Nair G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98024153; PubMed=9356471; McCherron A.C., Lee S.-J.; McCherron A.C., Lee S.-J.; "Double muscling in cattle due to mutations in the myostatin gene."; Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                            Genew; HGNC: 4223; GDF8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ma K., Ezzat S.,
Arver S., Bhasin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                         DISULFID
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                                                                                                                                                                                                         nterPro; IPR001839; TGFb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY) SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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                                                                                                                                                                                                                             601788;
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         24
267
281
309
313
Cytokine; Glycoptotein; Signal.

23 POTENTIAL.

14 266 POTENTIAL.

17 375 GROWTH/DIFFERENTIATION FACTOR 8.

18 340 BY SIMILARITY.

19 372 BY SIMILARITY.

19 374 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            muscle;
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         Query Match
Best Local Sim
Matches 109;
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                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                         HSSP; P18075; 1BMP
                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                             PROSITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9103;
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                                                                                                                                                                                                                                          SM00204; TGFB;
                                                                                                                                                                                                               factor;
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          Conservative
                                                                      AA;
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375
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374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meleagris gallopavo (Common turkey).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              042221;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98024153; PubMed=9356471; MCPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; T.
Pfam; PF00688; TGFb propeptide; 1.
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY; BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF019625; AAB86692.1; ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DEGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on A.C., Lee S.-J.;
muscling in cattle due to murations in the myostatin gene.";
atl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
                                                                                                                                                                                                                                                                                                                                                                          Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                          TGF BETA 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42750 MW;
                                                                                                                      42784 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 629; DB 1;
100.0%; Pred. No. 1.2e-62;
^ Mismatches 0;
100.0%; Score 629; DB 1; 100.0%; Pred. No. 1.2e-62; tive 0; Mismatches 0;
                                                                                                                                          POTENTIAL.

GROWTH/DIFFERENTIATION FACTOR 8.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . . .) (POTENTIAL)
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N-LINKED (GLCNAC. . .) (PO
                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                   D2AEAB732AEB4E77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375
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                                                       Length 375;
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      Indels
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                                                                                                                                                (POTENTIAL)
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      Gaps
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THE REPORT OF TH
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InterPro; p18075; lbmr.

InterPro; IPR0011839; TGFb.

InterPro; IPR001111; TGFb.N.

Pfam; pF00019; TGF-beta; 1.

Pfam; pF00688; TGFb propeptide; 1.

ProDom; pD000357; TGFb; 1.

R SMART; SM00204; TGFB; 1.

PROSITE; PS00250; TGF BETA 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDF8_PIG
018831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Daneau I., Silversides D.W.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

TISSUE-Skeletal muscle;

MEDLINE-98024155; PubMed-9356471;

MCPherron A.C., Lee S.-J.;

MCPherron A.C., Lee S.-J.;

"Double muscling in cattle due to mutations in the myostatin gene.";

Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yorkshire pigs.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metāzoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDF8 OR MSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-10 AND 36-375 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Skeletal muscle;
Voelker G.R., Conroy J.C., Wheeler M.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Porcine myostatin cDNA sequences: Duroc, Hampshire, Meishan and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267
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                                                                                                                                                                                                                                                                                                                                               L; AF019623; AAB86690.1; ...
L; AF188635; AAF02770.1; -...
L; AF188636; AAF02771.1; -...
L; AF188637; AAF02772.1; -...
L; AF033855; AAC08035.1; -...
L; AF093798; AAC62489.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUSCLE GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHQANPRGSAGPCCTFTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hampshire, Meishan, and Yorkshire;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            008689;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESDOW
             InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb propeptide; 1.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 387:83-90(1997).
-!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL MUSCLE GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=97284412; PubMed=9139826; McPherron A.C., Lawler A.M., Lee S.-J.; McPherron of skeletal muscle mass in mice by a new TGF-beta superfamily member.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                         HSSP;
                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                         entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute1eoscom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDF8 OR MSTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
                                                                                                                                       EMBL; U84005; AAC53167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CD-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 VHQANERGSAGECCTETKMSFINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
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                                                                                                                                                                                                                                                                                                                                            SUBURIT: HOMODIMER, DISGLIFIDE-LINKED (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND ADULT
SKELFTAL MUSCLE. WEEK EXPRESSION IN ADIPOSE TISSUE.
BYELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-COITUM IN
DRVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5. EXPRESSED IN THE
MYOTOME COMPARTMENT OF SOMITES. AT LATER STAGES OF DEVELOPMENT,
                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION CONTINUES IN ADULTHOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                           MGI:95691; Gdf8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                           P18075; 1BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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340
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374
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GROWH/DIFFERENTIATION FACTOR 8.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . . ) (POTENTIAL)
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Pred. No. 1.2e-62;
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                                                                                                                                                                                       moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 375;
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035312;
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15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
                                                                                                                                                                                                               ProDom; PD000357; TGFb; SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Skeletal muscle;
MEDLINE=98024153; PubMed=9356471;
McPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDF8 OR MSTN
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                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF019624; AAB86691.1; -. HSSP; P18075; 1BMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                        SIGNAL
                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                       Pfam; PF00688;
                                                                                                                                                                                                                                                                                            Pfam; PF00019; TGF-beta;
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InterPro; IPR001111; TGFb_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Double muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 VHQANPRGSAGPCCTPTKWSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUSCLE GROWTH
                                                                                                                                                            factor;
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                                                                                                                                                                                          PS00250; TGF BETA 1;
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                                                                                                                                                            Cytokine;
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                                                                                                                               Glycoprotein; Signal.
POTENTIAL.
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INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC, . .) (PO
POTENTIAL.

GROWH/DIFFERENTIATION FACTOR
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GROWTH/DIFFERENTIATION FACTOR 8.
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Pred. No. 1.2e-62;
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Query Match
Best Local Similarity
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Best Local
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InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb propeptide; 1
ProDom; PD000357; TGFb; 1.
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018828;
15-JUL-1999
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Skeletal muscle;
TISSUE-Skeletal muscle;
MEDILINE-98024153; PubMed-9356471;
MEDILINE-98024153; PubMed-9356471;
MCPherron A.C., Lee S.-J.;
Prouble muscling in cattle due to mutations in the myostatin gene.";
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
Proc. Natl. Specifically As A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                   SEQUENCE
                                                                                                                                                                                     Growth factor; SIGNAL
                                                                                                                                                                                                           Probom; PB000357; TGFB; 1.
SMART; SM00204; TGFB; 1.
SMART; SM00204; TGF BETA 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_
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                                                                                      DISULFID
                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                       EMBL; AF019619; AAB86686.1;
                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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                                                                                                                                                                                                    Cytokine; Glycoprotein; Signal.
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N-LINKED (GLCNAC. . .) (POT;
; 933043D8C8C3294B CRC64;
 Score 623; DB 1;
Pred. No. 5.8e-62
                                                                   N-LINKED (GLCNAC
                                                                                                   GROWTH/DIFFERENTIATION FACTOR BY SIMILARITY, BY SIMILARITY, BY SIMILARITY.
                                                                                  INTERCHAIN (BY SIMILARITY)
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Pred. No. 1.2e-62;
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                                                 7B49B90ACAB926EA CRC64;
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                Length 375;
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                                                                                           Matches
                                                                                                                                                                                         CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                         DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                              Growtn
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatice Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Ceta
Bovidae; Caprinae; Ovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-UIL-1999 (Rel. 38, Created)
15-UIL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 8 precursor (GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHEEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb.N.
Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE~98024153; PubMed=9356471; McPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327
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     267
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                                               1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uble muscling in cattle due to mutations in the myostatin gene.", c. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUSCLE GROWTH.
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  DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFLFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00688; TGFb propeptide; 1.
m; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF019622; AAB86689.1; -. P18075; 1BMP.
                                                                                              106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; PD000357; TGF
SM00204; TGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                        factor;
                                                                                                                        Similarity
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267
281
309
313
339
                                                                                              Conservative
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                                                                                                                                                                                            42827 MW;
                                                                                                                     98.4%;
97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor 8 precursor (GDF-8)
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                                                                                                                        Score 619;
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N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                              GROWIH/DIFFERENTIATION FACTOR BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                            1C36F3833BB11241 CRC64;
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                                                                                                                     .6e-61;
                                                                                                                                             DB 1;
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                                                                                                                                        Length 375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                         (POTENTIAL).
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Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Growth/differentiation factor 8 precur
GDF8 OR MSTN OR MH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. C
                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=21343337; PubMed=11451380;
Jeanplong F., Sharma M., Somers W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANTS MH LEU-94
STRAIN=Holstein; TISSUB=Skeletal muscle;
MEDLINE=98024153; PubMed=9356471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               018836; 018829;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piedmontese cattle.";
Genome Res. 7:910-916(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kambadur R., Sharma M., Smith T.P.
"Mutations in myostatin (GDF8) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Friesian; TISSUE=Muscle, a
MEDLINE=97458167; PubMed=9314496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
                   EMBL; AF019761; AAB81508.1; -.
EMBL; AF019620; AAB86687.1; -.
EMBL; AF320998; AAG48116.1; -.
HSSB; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Double muscling in cattle due to mutations in the myostatin gene."; Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McPherron A.C., Lee S.-J
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genomic organization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MUSCLE GROWTH.
SUBUNIT: HOWOIMER; DISULFIDE-LINKED (BY SIMILARITY).
SUBUNIT: HOWOIMER; DISULFIDE-LINKED (BY SIMILARITY).
TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING AND ADULT
SKKLETAL MUSCLE. HIGHEST LEVELS FOUND IN THE HINDLIMB MUSCLES
M. SEMIMEMBRANOSUS AND M.BICEPS FEMORIS; LOW LEVELS IN OTHER
                                                                                                                                                                                                                                                                                                                                                                         HINDLIMB MUSCLES.

DEVELOPMENTAL STAGE: WIDELY EXPRESSED THROUGHOUT DEVELOPMENT.

LOW LEVELS ARE FOUND UP TO DAY 29 EMBRYOS. LEVELS INCREASE FE

DAY 31 UP UNTIL LATE GESTATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: ACTS
                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                    DISEASE: DEFECTS IN GDF8 ARE THE CAUSE OF THE DOUBLE-MUSCLE PHENOTYPE OR MUSCULAR HYPERTROPHY (MH), AN AUTOSOMAL RECESSIVE DISEASE REAGURNTLY FOUND IN THE BELGIAM BLUE AND PIEDMONTESE CATTLE BREEDS. THIS DISEASE IS CHARACTERIZED BY AN INCREASED
                                                                                                                                                                                                                                                                NUMBER OF MUSCLE FIBERS (HYPERPLASIA), RESULTING MUSCLE MASS OF 20-25%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VHQANPKGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPGMVVDRCGCS 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q95N97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIFICALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220:31-37(2001).
SPECIFICALLY AS A NEGATIVE REGULATOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Somers W.G., Bass J.J., Kambadur R., I neonatal expression of the bovine m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .P.L., Bass J.J.;
in double-muscled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MH TYR-313 and Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
rsor (GDF-8)
                                                                                                                                                                                                                                                                                                                                                                                            EMBRYOS. LEVELS INCREASE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Myostatin)
                                                                                                                                                                                                                                                                                     IN AN INCREASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bovine myostatin
                                                                                                                                                                                                 EMBL outstation
                                                                                                                                                                                                              a collaboration
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Matches 107;
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DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
DISULFID
Mech. Dev. 80:185-189(1999).
-i- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                        09ZIW4; 09QX55; 09R221;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 11 precursor (Bone morphogenetic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT
CONFLICT
                               BMP/TGFbeta superfamily during mouse embryogenesis.";
Mech. Dev. 80:185-189(1999).
                                                                                                                                       McPherron A.C., Lawler A.M., Lee S.-J.; "Regulation of anterior/posterior patterning of the axial skeleton growth/differentiation factor 11.";
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth factor; Cytokine; GTycoprotein; Signal; Disease mutation. SIGNAL 1 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001111; TGFb N.
Pfām; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb propeptide;
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
                                                                                      MEDLINE=99173787; PubMed=10072786;
                                                                                                     SEQUENCE OF 75-405 FROM N.A.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                               Dev. Biol.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                     GDF11 OR BMP11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                         Nakashima M.,
                                                                                                                                                                                MEDLINE=99318097; PubMed=10391213;
                                                                                                                                                                                                                                                                                             MEDLINE=99177155; PubMed=10075854;
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090
                                                           Wakashima M., Toyono T., Akamine A., Joyner A., Expression of growth/differentiation factor 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                              Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BSDOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEGLOCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                               L.W., Wolfman N.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                           BMP expressed in developing mouse limb, spinal cord, and tail potent mesoderm inducer in Xenopus embryos.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00250;
                                                                                                                                                                                                                                          potent
                                                                                                                                                                                                                                208:222-232(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 AA;
                                                                                                                              22:260-264(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGF BETA 1; 1.
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2375
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                                                                                                                                                                                                                                                                                                                                                         Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42551 MW;
                                                                                                                                                                                                                                                                              Celeste A.J., Hattersley G., Hewick R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.

GROWTH/DIFFERENTIATION FACTOR 8.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
F -> L (IN MH; PIEDMONTESE BREED).
C -> Y (IN MEF. 1).
M -> T (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 618; ub ...
No. 2.1e-61;
                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84E1AB20650C05F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405
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                                                               RESULT 11
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Best Local
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DISULFID
DISULFID
CARBOHYD
            GDFB HUMAN STANDARD;
O95390; Q9UID1; Q9UID2;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                      CONFLICT
                                                    HUMAN
                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00250;
                                                                                                      357
                                                                                                                                                                                                       98;
                                                                                                                                                                                                                                                                                                                                                                                                                          factor;
                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                         405 AA;
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                       TGF_BETA_1; 1
                                                                                                                                                                                                                                                                                 213
370
402
404
369
92
75
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89.9%;
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267

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HSSP; PLOVER AND PROPERTY OF THE PROPERTY OF T
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EMBL; AF100904; AAC72853.1; JOINED.
EMBL; AF100905; AAC72853.1; JOINED.
EMBL; AF028337; AAF21633.1; JOINED.
EMBL; AF028335; AAF21633.1; JOINED.
EMBL; AF028335; AAF21633.1; JOINED.
EMBL; AF028336; AAF21633.1; JOINED.
EMBL; AF028336; AAF21633.1; JOINED.
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-!- SUBCULLULAR LOCATION: SCOTETED LINKED (BY SIMILARITY).
-!- SUBCULLULAR LOCATION: SCOTETED (Probable).
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD, INITIALLY DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALIZING TO REGIONS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADULT DENTAL PULP AND BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in convey use by and for commercial modified and this statement is not removed. Use by and for commercial modified and this statement is not removed. Use it is not commercial modified and this statement is not removed. Use it is not commercial modified and this statement is not removed. Use it is not commercial modified and the statement is not removed.
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                                                                                                                                                                                                                                          297 NLGLDCDEHSSESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHL
                                                                                                              61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                           1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
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VQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPGMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 581;
Pred. No. 2
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INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (PC
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BY SIMILARITY.
GROWITH/DIFFERENTIATION FACTOR 11.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A74E382710A14781 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
2.9e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
      405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                356
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                                                                                                                             Query Match
Best Local
                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDF11 OR BMP11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth/differentiation factor 11 precursor (Bone morphogenetic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Predom; PROMO0357; TGFB; 1.
SMART; SM00204; TGFB; 1.
SMART; SM00204; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF100907; AAC72852.1; -.
EMBL; AF028933; AAF21630.1; -.
EMBL; AF028934; AAF21631.1; -.
HSSB; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE-99318097; PubMed=10391213; McPherron A.C., Lawler A.M., Lee S.-J.; Regulation of anterior/posterior patterning of the axial skeleton by growth/differentiation factor 11."; Nat. Genet. 22:260-264(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gamer L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99177155; PubMed=10075854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Fetal brain;
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001839; TGFb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 603936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bev. Biol. 208:222-232(1999).
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1 DFGLDCDEHSTESRCCRYFLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYFHTHL 60
                                                                                                                          тосат
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT. PLAY CRITICAL ROLLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN. SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted (PX-Vobable). SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGNC: 4216; GDF11.
                                                                                                                          Similarity
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Human).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                           ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40, Last sequence update)
41, Last annotation update)
                                                                                                                                                                                                               45090 MW;
                                                                                                                   92.48;
                                                                                                                                                                                       POTENTIAL.

BY SIMILARITY.
BY SIMILARITY.
GROWTH/DIFFERENTIATION FACTOR 11.
GROWTH/DIFFERENTIATION FACTOR 11.
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POLY-ALA.
POLY-ALA.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (GLCMAC. . .) (POTENTIAL
N-LINKED (GLCMAC. . .) (POTENTIAL
N-LINKED GLCMAC. . .)
                                                                                               7; Mismatches
                                                                                                                      Score 581;
Pred. No. 3
                                                                                                                                                  DB 1; Length 407;
                                                                                               4; Indels
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GREE BRANK

DT 30-WW
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042222;
30-MAY-2000
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CARBOHYD
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Growth/differentiation factor 8 precursor (GDF-8) (Myostatin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'A'NN, ZUB-GENDALIS, TGFD.
InterPro, IPRO01111; TGFD N.
Pfam, PF00019; TGF-Deta; T.
Pfam, PF00688; TGFD propeptide;
Pfam, PF00688; TGFD propeptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98024153; PubMed=9356471; McPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; Provot.
SMART; SM00204; TGFB; 1.
SMARTE; PS00250; TGF BETA 1; 1.
PROPRIETE; PS00250; TGF BETA 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF019626; AAB86693.1; -. HSSP; P18075; IBMP.
                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZFIN; ZDB-GENE-990415-165; gdf8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Double muscling in cattle due to mutations in the myostatin gene."; Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                          266 DSGLDCDENSSESRCCRYPLTVDFEDFGWDWIIAPKRYKANYCSGECDYMYLQKYPHTHL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VHQANPRGSAGPCCTFTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                             1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY). SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUSCLE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQQANPRGSAGPCCTPTKMSPINMLYFNDKQQLIYGKIPGMVVDRCGCS 407
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 letal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Danio.
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(Rel. 39, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                      90.6%; Score 570; DB 1; Lo
88.1%; Pred. No. 4.5e-56;
Mismatches 2;
                                                                                                                                                                                                                                                                                                                        42060 MW;
                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                            GROWTH/DIFFERENTIATION FACTOR 8. BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
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                                                                                                                                                                                                                                                                                                                           6302BC6C86562576 CRC64;
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                                                                                                                                                                                                                                                                  Length 374;
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                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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326 VNKASPRGTAGPCCTPTKMSPINMLYFNGKEQIIYGKIPSMVVDRCGCS 374

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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakashima M., Toyono T., Akamine A., Joyner A.;
"Expression of growth/differentiation factor II., a new member of the
BMP/TGEDeta superfamily during mouse embryogenesis.";
Mech. Dev. 80:185-189(1999).

-i- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
DIENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
TISSUES AND IN ESTABLISHING THE SKELTTAL PATTERN (BY SIMILARITY).

-i- SUBBURIT: HOWODIMER, DISTULPIDE-LINKED (BY SIMILARITY).

-i- SUBBURIT: HOWODIMER, DISTULPIDE-LINKED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDF11 OR BMP11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Growth/differentiation factor 11 precursor (Bone morphogenetic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb propeptide; 1.
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF092733; AAD05266.1; -. HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99173787; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDFB_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00204; TGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
                303 VQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPGMVV 345
                                                                                                243 NLGLDCDEHSSESRCCRYPLTVDFEASGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHL 302
                                                        61
                                                                                                                                                                                                   Local
                                                                                                                             1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                     VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVV 103
                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00250;
                                                                                                                                                                                                                                                                                                         243
154
257
315
38
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                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10072786;
                                                                                                                                                                                                 84.9%;
                                                                                                                                                                                                                                                              39094 MW;
                                                                                                                                                                                                 Score 534; DB 1;
Pred. No. 4.2e-52;
                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
GROWTH/DIFFERENTIATION FACTOR 11.
FOLY-GIY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                  INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (PC
                                                                                                                                                                                                                                                              81D5B93FED6B0443 CRC64;
                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 AA.
                                                                                                                                                                                                                    Length 345;
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                Gaps
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RESULT 14
IHBB_MOUSE
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MGD; MGI:96571; Inhbb.
InterPro; IPR001183; TGFb.
InterPro; IPR00111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00068; TGFb propeptide; 1
ProDom; P0000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJNE 93321614; PubMede 9330535;
Albano P.M., Groome N., Smith J.C.;
Albano P.M., Groome N., Smith J.C.;
Albano P.M., Groome N., Smith J.C.;
Partivins are expressed in preimplantation mouse embryos and in ES and EC cells and are regulated on their differentiation.";
Development 117:711-723(1993).
Perelopment 117:711-723(1993).
PERSPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
INHIBLINE/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, GRAYTHOLD DIFFERENTIATION, IGUILIN SECRETION, MERRY CELL SURVIVAL,
EMBRYCONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR EMBRYCONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR EMBRYCONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR EMBRYCONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR EMBRYCONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR EMBRYCONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR EMBRYCONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR EMBRYCONIC CANADA BY THE PROPERTY OF THE PROPERTY
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01-FBB-1994 (Rel. 28, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1nhibin beta B chain precursor (Activin beta-B chain) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ACTIVINS.

IS SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.

INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

ACTIVIN A IS A HOMODIMER OF BETA-A.

ACTIVIN B IS A HOMODIMER OF BETA-A.

ACTIVIN B IS A HOMODIMER OF BETA-A.

ACTIVIN B IS A HOMODIMER OF BETA-B.

ACTIVIN B IS A DIMER OF BETA-B.

ACTIVIN B IS A HOMODIMER OF BETA-B.

ACTIVIN 
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Mech. Dev. 50:229-245(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CBA X NMR1; TISSUE=Testis;
MEDLINE=95344997; PubMed=7619733;
Rityos O., Tuuri T., Eramaa M., Sainio K., Hilden K., Saxen L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                 PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Hormone; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X83376; CAA58290.1; -. EMBL; X69620; CAA49326.1; -. PIR; S31441; S31441.
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                                                                                                           IHBB_MOUSE
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POTENTIAL.
INHIBIN BETA B CHAIN.
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DVR1_BRAR
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Best Local (
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VG1 OR DVR-1 OR DVR-1.
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniforme Cyprinidae; Danio.
NCB1_TaxD=7955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
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P35621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heide K.A., Grunwald D.J.;
"The DVR-1 ('91) transcript of zebrafish is maternally supplied and distributed throughout the embryo.";
Dev. Biol. 159:418-426(1993).

PROCITION: SERVES TO FACILITATE THE DIFFERENTIATION OF BITHER AS A COFACTOR IN AN INSTRUCTIVE SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT.
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: HOMODIMER (PROBABLE).

-!- TISSUE SPECIFICITY: ABUNDANT IN OVARIES AND EGGS, AND EQUALLY
-IDISTRIBUTED ANONG ALL BLASTOMERES.
-!- DEVELOPMENTAL STAGE: CONCENTRATED IN THE STREAMING CYTOPLASM IN
JUST-PERTILIZED EGGS. EVENLY PARTITIONED DURING CLEAVAGE ANONG ALL
BLASTOMERES. ASSENT IN THE YOLK CELL DURING CLEAVAGE, BLASTULA AND
GASTRULA STAGES. DISTRIBUTED HOMOGENEOUSLY AMONG ALL CELLS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
InterPro; IPR002400; GF cysknot.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00089; TGF-beta; I.
Pfam; PF00089; TGF-beta; I.
Pfam; PF00089; TGF-bropptide; 1.
                                                                                                   EMBL; U00931; AAC27347.1; -. HSSP; P12643; 3BMP. ZFIN; ZDB-GENE-980526-389; dvrl.
                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94009920; PubMed=8405668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 FHTAVVNOYRMRGLNPGPVNSCCIPTKLSSMSMLYFDDEYNIVKRDVPNMIVEECGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 GLECDGRT--SLCCROOFFIDERLIGWNDWIIAPTGYYGNYCEGSCP-AYLAGVPGSASS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 -HTHLVHQANDRG-SAGD----CCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP---- 56
                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 BY SIMILARITY.
220 BY SIMILARITY.
252 BY SIMILARITY.
254 BY SIMILARITY.
254 BY SIMILARITY.
219 INTERCHAIN (BY SIMILARITY).
219 H -> D (IN REP. 2).
315 H -> D (IN REP. 2).
3178 MW; 2524B2IDC648D9A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.48;
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BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
H -> D (IN REF. 2).
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Pred. No. 2e-20;
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Best Local
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                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                      Probom; PD000357; TGFb; 1.
SMART; SM00204; TGF; SM0250; TGF BETA 1; 1.
Growth factor; Mitogen; Glycopro
                                                                                                                                                                                                             DISULFID
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                                                                                                                                                                                   CARBOHYD
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                                                   249
309 SFDPKGTPOPCCVPIKLSPISMLYYDNNDNVVLRHYEDMVVDECGC 354
                                                                          11 TESRCCR-YPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYPHTH-----LVH 62
                        63 QANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGC 108
                                                  TPSNVCKPRRLYIDFKDVGWQDWIIAPQGYLANYCHGECPFPLSESLNGTNHAILQTLVH 308
                                                                                                                   Similarity
                                                                                                                                                          355 AA;
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                        Mitogen; Glycoprotein;
                                                                                                                39.1%;
                                                                                                                                                          40201 MW; 0ED5B9850EBFB222 CRC64;
                                                                                                     16;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . . ) (POTER
                                                                                                                Score 246; DB 1; Length 355; Pred. No. 4.7e-20;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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DVR-1 PROTEIN
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                                                                                                       Mismatches
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Search completed: January 31, 2003, 18:21:31 Job time: 9.5 secs

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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                          Score
   629
629
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5644
                                                                                                                                                                                                                                                                                                                 SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_nwarn:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
11: sp_vertebr
12: sp_virus:*
13: sp_vertebr
14: sp_unclass
15: sp_rotheap
16: sp_acteri
17: sp_archeap
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Match
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Gapop 10.0 , Gapext 0.5
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629
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Copyright (c) 1993 - 2003 Compugen Ltd.
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sp_organelle:*
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Q9GM97
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Q90YY0
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Q90ZD2
Q90ZD1
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O9tsy2 sus scrofa
C9gm97 equus cabal
C95986 macaca fasc
C8uwd8 columba liv
C8uwd7 coturnix ch
C98sp0 gallus gall
C98sp0 gallus gall
C9wm96 boss taurus
C9mm16 capra hircu
C9mm86 boss taurus
C95n11 capra hircu
C9mm18 ovis aries
C90yy0 ictalurus p
C9m20 gonocriynchu
C9d18 salmo salar
C902d2 conocriynchu
C90zd1 oncoriynchu
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5	44	43	42	41	40	9	38	37	36	35	34	S S	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
226.5	230.5	236.5	236.5	239.5	239.5	239.5	240.5	241.5	241.5	242	254	259	286	301.5	301.5	302	311	394	529	543	554	557	559	562	563	564	564	564
36.0	36.6	•	•	38.1	•	•	•		•	38.5	•	•	45.5	•	47.9	•	49.4	62.6		86.3	•			89.3			89.7	89.7
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## ALIGNMENTS

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Query Match 100.0%; Score 629; DB 6; Length 162; Best Local Similarity 100.0%; Pred. No. 1e-65; Matches 109; Conservative 0; Mismatches 0; Indels 0;	SQ SEQUENCE 162 AA; 18290 MW; FE3535334512856E CRC64;				InterPro; IPR001839; TG	InterPro; IPR002400;	DR HSSP: P18075; 1BMP.	-!- SIMILARITY: BELONGS TO	Anim. Genet. 30:468-470	myostatin (GDF8; MSTN) gene.";			RY MEDITINE=20078370. Primpd=10613246;		NCBI_TaxID=9823;	Mammalia; Butheria; Cetartiodactyla; Suina; Suidae;	OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	Cha carofa		01-JUN-2002 (TrEMBLrel. 21, Last	01-MAY-2000 (TrEMBLrel. 13,		Q9TSY2;	ID OSTSY2 PRELIMINARY: PRT: 162 AA.	RESULT 1
Gaps																	•								

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Q95J86
ID Q95J
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DT 01-D
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EN MACA
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InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb propeptide; 1
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                           Q95J86; PRELIMINARY;
Q95J86; UTEMBLE. 19,
01-DEC-2001 (TEMBLE. 19,
01-JUN-2002 (TEMBLE. 21,
                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Cercogithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein.
SEQUENCE 375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hosoyama T., Yamanouchi K., Tojo H., Tachi C.;
"Molecular cloning of equine myostatin cDNA and serum level
myostatin in horse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9GM97;
01-MAR-2001
                                             NCBI_TaxID=9541;
                                                                                                                                                   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
                                                                                                                                                                                Myostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00018; EF_HAND; UNKNOWN_1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB033541; BAB16046.1; -.
HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Equus caballus (Horse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002048; EF-hand.
InterPro; IPR001839; TGFb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Equus caballus (Horse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFGLDCDEHSTESRCCRYPJTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42736 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 629; DB 6; 100.0%; Pred. No. 2.4e-65; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16,
16,
21,
                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                             Vertebrata; Eutele
i; Cercopithecidae;
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                                                                                                                     Euteleostomi;
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A Smock S.L., Owen T.A.;

A Smock S.L., Owen T.A.;

A Smock S.L., Owen T.A.;

Cloning of the open reading frame DNA for macaque fascicularis ("Cloning of the open reading frame DNA for macaque fascicularis in the control of the EMBL/GenBank/DDBJ databases.

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

C --- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

REMBL, AYOS5750, AAL17640.1; --

REMBL, AYOS5750, AAL17640.1; --

RE InterPro; IPR00183; TGFb.

RE InterPro; IPR00183; TGFb N.

RE InterPro; IPR001111; TGFb N.

RE Pfam; PF00019; TGF-beta; I.

RE Pfam; PF00019; TGF-beta; I.

RE Pfam; PF00018; EF-HAND; UNKNOWN 1.

RE PROSITE; PS00018; EF-HAND; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                    A Gu Z., Yang W., Cheng Z., Li H., Zhu D.;

"Molecular Cloning and Tissue Distribution of the Myostatin Gen
T Duck, Goose, Pigeon and Quail.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, AF440863, AAL35277.1; -.

R InterPro; IPR001839; TGFb
R InterPro; IPR001839; TGFb
N.
Pfam; PF00019; TGF-beta; I.

R Pfam; PF00688; TGFb propeptide; 1.

R Pfam; PF00688; TGFb; 1.

R ProDom; PD000357; TGFb; 1.

R PROSITE; PS00018; EP HAND; UNKNOWN 1.

R PROSITE; PS000250; TGF BETA 1; UNKNOWN 1.

R PROSITE; PS000250; TGF BETA 1; UNKNOWN 1.
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Best Local :
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01-MAR-2002
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Columba livia (Domestic pigeon).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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SEQUENCE 375 AA;
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327
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                                                                                                                                                              1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                   VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                      DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
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                                                                                                                                                                                                                      109;
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                                                                                                                                                                                                                      Conservative
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Last annotation updat
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Pred. No. 2.4e-65;
                                                                                                                                                                                                                                              Score 629; DB 13;
Pred. No. 2.4e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2149B46AC7D446E7 CRC64;
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RESULT 6
            DRRRRRRR OXCOCCONDITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                           development.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; AF346599; AAK18000.1; -.
EMBL; AF346599; BMP.
InterPro; IPR000048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8UWD7 PRELIMINARY;
QBUWD7;
Q1-WAR-2002 (TIEMBLrel. 20,
01-MAR-2002 (TIEMBLrel. 20,
01-JUN-2002 (TIEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O98SPO PRELIMINARY;
O98SPO;
O1-JUN-2001 (TrEMBLrel. 17,
O1-JUN-2001 (TrEMBLrel. 17,
O1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Wolecular Cloning and Tissue Distribution of the Myostatin Gene Duck, Goose, Pigeon and Quail.";
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF440864; AN135278.1;
InterPro; IPR001839; TGFb.
InterPro; IPR001819; TGFb.
InterPro; IPR00187; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000357; TGFb; 1.

SMART; SM00204; TGFB; 1.

PROSITE; PS00018; EE HAND; UNKNOWN 1.

PROSITE; PS00250; TGF BETA 1; UNKNOWN 1.

SEQUENCE 375 AA; 42721 MW; B893B1TA42DE0725 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                            Zhang Y., Yang W., Zhu D.; "Genomic structure and expression of the chicken GDF-8 during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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         IPR001839;
IPR001111;
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Last sequence update)
Last annotation update)
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Last annotation update)
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D1 01-M
D1 01-M
D2 01-M
D3 MY08
GN MSTN
GN MSTN
GN MSTN
GN MSTN
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Best Local :
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Best Local
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Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
Wholecular Cloning and Tissue Distribution of the Myostatin Gene in
Duck, Goose, Pigeon and Quail.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP440862; AAL35276.1;
InterPro; IPR002048; EF-hand.
InterPro; IPR001839; TGFb
InterPro; IPR001839; TGFb N.
Pfam; PF00019; TGF-beta; I.
Probon; PD000357; TGFb; 1.
PROCATE: ESCANTE: 
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Pfam; PF00668; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00018; EF HAND; UNKNOWN_1.
PROSITE; PS00250; TGF_BETA_1; 1.
QBUWEO PRELIMINARY;
QBUWEO;
Q1-MAR-2002 (TrEMBLrel. 20,
Q1-MAR-2002 (TrEMBLrel. 20,
Q1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBUWD9;
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SEQUENCE 375 AA; 42717 MW; D980E286426E4D4F CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
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PROSITE; PS00250; TGF BETA 1; UNKNOWN 1.
SEQUENCE 375 AA; 42667 MW; 57DDE49D3AA2978C CRC64;
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Created)
Last sequence update)
Last annotation update)
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"Molecular Cloning and Tissue Distribution of the Myostatin Gene in UT Duck, Goose, Pigeon and Quail.";

Submitted (OCT-2001) to the EMEL/GenBank/DDBJ databases.

RE EMBL, AF440861; AA135275.1; --.

RE InterPro; IPRO01839; TGFb.

IN InterPro; IPRO01839; TGFb.

IN InterPro; IPRO01811; TGFb. N.

Pfam; PF00018; TGFb-propeptide; 1.

PFADDOM; PD000557; TGFb; 1.

SMART; SM00204; TGFB; 1.

PROSITE; PS00018; EF HAND; UNKNOWN 1.

PROSITE; PS00018; EF HAND; UNKNOWN 1.

SEQUENCE 375 AA; 42817 MW; 1BA7FF5225C23620 CRC64;
                                                                                                                                          Best Local Similarity 98.3
Matches 107; Conservative
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Best Local Similarity
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01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                    Shibata M., Muramoto T., Aikawa K.;

"Genomic organization and sequence of the myostatin gene in bovine.";

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB076403; BAAF9498.1; -.

InterPro; IPR002048; EF-hand.

InterPro; IPR0021839; TGFb
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; 1.

Pfam; PF00019; TGF-beta; 1.

PF000m; PD000157; TGFb; 1.

SMART; SM00204; TGFB; 1.

PROSITE; PS00250; TGF BETA 1; UNKNOWN 1.
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Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 DÉGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSEECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VHQANPRGSAGECCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
1 DFGLDCDEHSTESRCCRYPLTVDREAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 20, (TrEMBLrel. 20, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                    98.3%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.7%; Score 621; DB 13; 99.1%; Pred. No. 2.1e-64;
                                                                                                                                               ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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Last annotation update)
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                                                                                                                                          Score 618; DB 6; L
Pred. No. 4.6e-64;
l; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375
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                                                                                                                                                                                                                                    Length 375;
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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NON_TER
NON_TER
189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lian Z., Pan Q., Chen H., Jin H., Li N.;

"Cloning of intron 2 of the myostatin gene in goat.",

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY BELONGS TO THE TGF-BETA FAMILY.

EMBL, AY022689, AR469790.1;

InterPro; IPR001839; TGFD.

InterPro; IPR001839; TGFD.

PEam; PF00019; TGF-beta; 1.

PEam; PF00088; TGFD propeptide; 1.

PF00m; PD000357; TGFb 1.

PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                     O9MZ18;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q95N11;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2002 (TrEMBLrel. 21,
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Lian Z., Jin H., Li N.;

"Cloning of intron 2 of the myostatin gene in sheep.";

Submitted (MAY-2000) to the ENBL/GenBank/DDBJ database

-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

EMBL; AF266758; AAF78069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q95N11
                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                           Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81ZM6D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Capra hircus (Goat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myostatin (Fragment).
                                                                                                                                                                                                                                       Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                    Myostatin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9925;
                                                                                                                                                                                                         NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 DFGLDCDEHSTESRCCRYPLTVDPBAFGWDWIIAPKRYKANYCSGECEFLFLQKYPHTHL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185
; 20953 MW; 03675B386E9D64D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2,
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 606; DB 6;
Pred. No. 5.7e-63;
2; Mismatches 1
                                                                                                                                                                                                                                                                     Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                   databases
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RESULT 12
Q90YY0
ID Q90YY
AC Q90YY
DT 01-DE
DT 0
                                               RESULT 13
Q90W05
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Best Local S
Matches 97
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Best Local Sim
Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Kocabas A.M., Liu Z.J.;

"Molecular characterization and expression of the myostatin general catfish (Ictalurus punctatus).";

T channel catfish (Ictalurus punctatus).";

L Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

C -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

REMBL, AF396747; AAK84666.1; -.

REMBL, AF396747; AAK84666.1; -.

R InterPro; IPR001131; TGFb N.

R InterPro; IPR001111; TGFb N.

R InterPro; IPR001111; TGFb N.

R Ffam; PF00619; TGF-beta; I.

R Pfam; PF00619; TGF-beta; I.

R Pfam; PF00619; TGF-BeTA 1; UNKNOWN 1.
Q90W05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Totalurus punctatus (Channel catfish).
Bukaryota, Metazoa, Chordata, Craniata,
Actinopterygii, Neopterygii, Teleostei,
Ictaluridae, Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb propeptide; 1.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Kocabas A.M., Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myostatin.
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                                                                                                                                                    343
                                                                                                                                                                                                                                                         283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139
                                                                                                                                                                             63 QANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109 :|||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                        ω
                                                                                                                                                                                                                                                   GLDCDENSSESRCCRYPLTVDFEDFGWDWIIAPKRYKANYCSGECDYVHLQKYPHTHLVN 342
                                                                                                                                                                                                                                                                                     GLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHLVH 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCG 107
                                                                                                                                                 KANPRGTAGPCCTPTKMSPINMLYFNGKEQIIYGKIPSMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHQANPKGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPGMVVDRCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFGLDCDVHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFLFLQKYPHTHL 138
                                                                                                                                                                                                                                                                                                                                                           97;
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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185
185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             389 AA; 43600 MW; 569FB952B7E9E173 CRC64;
                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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20923 MW;
                                                                                                                                                                                                                                                                                                                                                                           90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.2%; Score 599; DB 6; Length 185; 96.3%; Pred. No. 3.8e-62;
                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                              Score 570; DB 13
Pred. No. 2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3.86
2; Mismatches
                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                      385
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Ostariophysi; Siluriformes;
                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
                      8
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 389;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9DDI8;
                                                                                                                                                                                                                                                                                      Salmo salar (Atlantic salmon).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopoterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sparus aurata: sequence, genomic structure, and expressis submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; AF258448; AAK53545-1; --
EMBL; AF258447; AAK53544-1; --
EMBL; AF26847; AAK53544-1; --
EMBL; AF26848; TGFb NAK53544-1; --
EMBL; AF26848; TGFb NAK53544-1; --
EMBL; AF26848; TGFb Dropeptide; 1.
"The two myostatin genes of Atlantic salmon (Salmo salar) expressed in a variety of tissues."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                          Ostbye T.K., Galloway T.F., Nielsen C., Gabe "The two myostatin genes of Atlantic salmon expressed in a variety of tissues.";
Submitted (DEC-2000) to the EMBL/GenBank/DDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sparus aurata (Gilthead sea bream).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                             Ostbye T.K., Galloway T.F.,
Andersen O.;
                                                                                                                                                                                                                                                                   NCBI_TaxID=8030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     Myostatin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patarnello T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maccatrozzo
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                                                                              SEQUENCE FROM N.A.
                                                                                                             Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of the myostatin gene in the gilthead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 DSGLDCDENSPESRCCRYPLTVDFEDFGWDWIIAPKRYKANYCSGECEYMHLQKYPHTHL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNKANPRGSAGPCCTPTKMSPINMLYFNRKEQIIYGKIPSMVVDRCGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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89.9%;
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18,
21,
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19,
21,
                                                            Nielsen C.,
                                                                                                                                                                          EMBL/GenBank/DDBJ
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 567; DB 13;
Pred. No. 4.4e-58;
6; Mismatches 5;
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Last annotation update)
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                                                                Gabestad I., Bardal T.,
                                                                                                                                                                                                        Gabestad I., Bard
Lmon (Salmo salar)
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                                                                                                                                                                                                                                                                                                                                                                                            EPSEQUENCE FROM N.A.

RESCAIR P.-Y., Jutel I., Ralliere C.;

RR rescair P.-Y., Jutel I., Ralliere C.;

RT "Two myostatin genes are differentially expressed in myotomal muscle

RT of the trout (Oncorhynchus mykiss).";

RL J. Exp. Biol. 0:0-0(2001).

CC -[-SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

CR EMBL; AF273035, AAK71707.1; -.

DR InterPro; IPR001839; TGFb.

DR InterPro; IPR001839; TGFb.

DR InterPro; IPR001839; TGFb.

DR Pfam; PF00018; TGF-betta; 1.

DR Pfam; PF00088; TGFb propeptide; 1.

DR PROSITE; PS000250; TGF-BETA_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 89.7%;
Best Local Similarity 89.0%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb propeptide; 1.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS000250; TGF BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                           Glycoprotein.
SEQUENCE 373 AA; 42049 MW; 9DD4771B5CF671EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myostatin 1.

Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

Dukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q90ZDZ PRELIMINARY; PRT; 373 AA.
Q90ZDZ]
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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CHAIN 265 373 MYOSTATIN.
SEQUENCE 373 AA; 41896 MW; C641D71D83E66C4D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. EMBL; AJ297267; CAC19541.2; -. EMBL; AJ316006; CAC59700.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P12643; 3BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 VMKANERGTAGPCCTPTKMSPINMLYENRKEQIIYGKIPSMVVDRCGCS 373
                                    61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                               97;
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                            89.7%; Score 564; DB 13; Length 373;
89.0%; Pred. No. 9.5e-58;
rative 7; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 564; DB 13;
Pred. No. 9.5e-58;
7; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 373;
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                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Search completed: January 31, 2003, 18:21:08

Job time : 27 secs

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Regult
No.
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
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                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Geneseq 101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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10: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA199.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
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453.885 Million cell updates/sec
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  AAB20141
AAM51935
AAR63161
AAW69883
AAY15386
AAB73182
AAB73189
AAB20153
AAB20153
                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                   Human growth diffe Human ToFbeta prot Mouse growth diffe Murine growth diffe C-terminal region Murine GDF-8 #1.
Rat GDF-8. Rattus Growth differentia Chicken GDF-8. Ga
                                                                                                                                                                                                                                                                        Description
  Growth differentia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
AAB20141
     Increasing the muscle mass of animals used in meat production by down regulating growth differentiation factor 8 (\mathrm{GDF-8}) activity in the
                                                                                                                                                                                                                         20-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB20141;
                                                                        WPI; 2001-112680/12.
                                                                                                                       Halkier T, Mouritsen S,
                                                                                                                                                                          (MEBI-) M & E BIOTECH AS.
                                                                                                                                                                                                                                                                                                  20-JUL-2000; 2000WO-DK00413.
                                                                                                                                                                                                                                                                                                                                                    25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                      WO200105820-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB20141 standard; Protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                         99DK-0001014
99US-0145275
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29 100.0 375 23 AAU7562	29 100.0 375 23 AAU	29 100.0 375 23 AAUT	29 100.0 375 23 AAE1	29 100.0 375 23 AAEI	29 100.0 375 23 AAEI	29 100.0 375 2	29 100.0 375 22 AAB	29 100.0 375 22 AAB:	29 100.0 375 22 AAB;	29 100.0 375 22 AAB	29 100.0 375 21 AA1	29 100.0 375 21	29 100.0 375 21 AAB2	29 100.0 375 20	29 100.0 375 20	29 100.0 375 20	29 100.0 375 20	29 100.0 375 20	629 100.0 375 20 AAY33932	29 100.0 375 20	29 100.0 375 20	29 100.0 375 20	29 100.0 375 20	29 100.0 375 20	29 100.0 375 20 AAY3	29 100.0 375 20 AAY33	29 100.0 375 20 AAY32	29 100.0 375 19 AAW65	29 100.0 375 19 AAW69	29 100.0 375 19 AAW69	29 100.0 375 19 AAW6	29 100.0 375 15 AAR63	29 100.0 374 23 AAUT	27 100.0 302 22 MADE
 п.	Porcine promyostat	Human promyostatin	Meleagris gallopav	Porcine promyostat	Chicken promyostat	Human promyostatin	Pig growth differe	Chicken growth dif	iff	#2.		Human growth diffe	GDF-8.	Human myostatin.	Turkey GDF-8 prote	Chicken GDF-8 prot	ឆ្ន	Œ	acid			acid				8	Amino acid sequenc	growth dif	n growth diff	æ	ken gr	H	n promyost	STORES GAL

## ALIGNMENTS

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Growth differentiation factor 8; GDF-8; myostatin; down-regulation; vaccine; muscle; meat; cachexia; cardiant; human; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human growth differentiation factor 8 C-terminal region.
Klysner S;
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animal through induction of anti-GDF-8 antibody production

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence comprises the 109 amino acid residue CC C-terminal region of human growth differentiation factor 8 (GDF-8), i.e. residues 267-375 of the full-length protein (see AAB20131). The homodimer of this region is thought to be the biologically active form of GDF-8. It is an object of the muscle civentian to produce a recombinant therapputic vaccine capable of convention to produce a recombinant therapputic vaccine capable of ceffecting down-regulation of GDF-8 in order to increase the muscle composite the control of the muscle composite the control of GDF-8 (see AAB20145-53) are provided that are capable of breaking autotolerance against course in which a portion of the native sequence is replaced by a course of the protein of the native sequence is replaced by a course of the high number (9) of Cys residues in the C-terminal course in the control of the native sequence in the creating can be used for genetic immunisation of the native 3-dimensional course tructure of the protein. Nucleic acids encoding the GDF-8 variants can be used for genetic immunisation of the antimals. Down-regulation confidence is activity can increase muscle mass by up to at least 45% in control of the course of the course of the activity can increase muscle mass by used to a treat human diseases such as canti-GDF8 vaccines can be used to control of the activity and for nations a canter and absorbed atrophy is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                           Human; TGFbeta; transforming growth factor beta; mutant; antagonist; agonist; ectopic bone formation; psoriasis; muscular atrophy; scar; formation; fibrosis; oirthosis; osteopathic; antipsoriatic; antifibrotic; hepatotropic; vulnerary; GDF8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
  WPI; 2002;042559/06
                                    Sebald W, Nickel J;
                                                                                                                                                                                            06-DEC-2001.
                                                                                                                                                                                                                                   DE10026713-A1.
                                                                                                                                                                                                                                                                                                                                                                                                           Human TGFbeta protein superfamily protein GDF8.
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM51935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM51935 standard; protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 93-94; 110pp; English.
                                                                              (SEBA/) SEBALD W.
                                                                                                                   30-MAY-2000; 2000DE-1026713
                                                                                                                                                       30-MAY-2000; 2000DE-1026713.
                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pronounced and for patients suffering from acute and chronic heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 629; DB 22;
100.0%; Pred. No. 2.8e-60;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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New mutein of transforming growth factor-beta superfamily protein, useful for treating or preventing e.g. ectopic bone formation, competes
                                                                                                        for receptor binding
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Disclosure; Fig 6; 54pp; German.

The present invention relates to muteins of a chain of a protein which, when in the form of a homodiner, has antagonistic or partial agonistic activity, and where the mutation results in the protein binding with low affinity to its receptor. The protein is a member of the transforming growth factor beta (TGFbeta) superfamily. The mutant sequences of the invention can be used in the treatment of diseases associated with the overexpression of TGFbeta family proteins, including ectopic bone formation, psoriasts, muscular atrophy, sear formation, fibrosis and cirrhosis. The present sequence is the human GDF8 protein.

Sequence 109 AA;

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                                                         В
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                                                                                                                   Matches
                                                                                                                                 Query Match
Best Local
61
                            61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                         1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                         DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                  109;
                                                                                                                                   Similarity
                                                                                                                   Conservative
                                                                                                                               100.0%;
                                                                                                                  0; Mismatches
                                                                                                                               Score 629; DB 23;
Pred. No. 2.8e-60;
                                                                                                                     0
                                                                                                                     Indels
                                                                                                                                             Length 109;
                                                                                                                  0;
                                                                                                                  Gaps
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0,

AAR63161 RESULT 3 AAR63161 standard; Protein; 126 AA

23-JUN-1995 (first entry)

adipocyte; obesity; transforming growth factor-beta. Growth differentiation factor-8; GDF-8; cell proliferation; Mouse growth differentiation factor-8 partial sequence.

Mus musculus

WO9421681-A.

29-SEP-1994.

18-MAR-1994; 94WO-US03019.

19-MAR-1993; 93US-0033923.

(UYJO ) UNIV JOHNS HOPKINS SCHOOL MED

Lee S, Mcpherron AC

1994-316943/39.

Q-PSDB; Q76380.

New growth differentiation factor 8 - useful for treatment and diagnosis of cell proliferative disorders esp. of muscle.

Disclosure; Page 41; 84pp; English

GDF-8 can be used to maintain cells before transplantation; to improve efficiency of cell fusion and to treat obesity or diserelated to abnormal adipocyte proliferation.

126 AA;

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ARBSULT 4
ARAWAS PRINCIPAL
AND SANG
AC AANG
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This is the amino acid sequence of the C-terminal portion of mouse growth differentiation factor-8 (GDF-8), a novel member of the transforming growth factor-beta superfamily that appears to relate to various cell proliferative disorders, especially those involving muscle, nerve and adipose tissue. The sequence was deduced from a partial genomic clone (see AAV45809). A full-length sequence (see AAW30689) has been deduced from a cDNA clone (see AAV42113). The invention provides novel mammalian and avian GDF-8 proteins (see AAW5983-92). A transgenic non-human animal is claimed in which CDF-8 expression is disrupted or interfered with. Also claimed are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb from these animals; (2) method for increasing muscle mass in animals by administering an antibody (Ab) that binds to GDF-8; (3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Growth differentiation factor-8; GDF-8; mouse; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contents, also use of GDF-8 inhibitors for treating cancer, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV45809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-1997;
05-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 58; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuromuscular disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McPherron AC;
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97US-0795071.
97US-0847910.
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16..17
17..126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "mature polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 126;
                                                                                                                                                                                                                                                                                         involving
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibiting the action of GDF-8 by treating foetal or adult muscle or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic acid encoding a GDF-8 protein truncated by loss of the C-terminal cardive fragment. The transgenic animals have increased muscle mass and for poultry reduced cholesterol contents. Method (3) is used to treat muscle wasting or neuromuscular diseases, muscular atrophy cand aging, particularly muscular dystrophy, spinal cord or transmatic injuries, congestive or obstructive lung disease, AIDS and cachexia. Method (4) is used to treat cancer of muscle, connective tissue and bone, or obesity. Also (not claimed) GDF-8 connective tissue and bone, be used to treat cancer of muscle, cambe used to maintain myoblasts intended for transplanting or to improve efficiency of fusion. Ab can be used to detect and cancer of particularly in muscle, for diagnosis or monitoring), also for immunotherapy and in vivo imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth differentiation factor; tissue growth; muscle growth; cell differentiation; animal feed; muscle disorder; bone degeneration; nerve degeneration; GDF-8; development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY15386;
                                                                 WPI; 1999-494289/41.
N-PSDB; AAZ06446.
                                                                                                                                                                                                                                                                                                                                                                                              Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-terminal region of mouse Growth Differentiation Factor-8 (GDF-8).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY15386 standard; Protein; 126 AA
                diseases
                                New differentiation factor useful for treating neurodegenerative
                                                                                                                                                                                                28-JUL-1998;
05-FEB-1998;
                                                                                                                                                                                                                                                   05-FEB-1999;
                                                                                                                                                                                                                                                                                      12-AUG-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transforming growth factor beta; TGF-beta.
                                                                                                                                                           (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECBFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                98US-0124180.
98US-0019070.
                                                                                                                                                                                                                                                   99WO-US02511
                                                                                                                                                                                                                                                                                                                                                                                              /label= Potential_proteolytic_cleavage_site
16..17
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
13..14
                                                                                                                                                                                                                                                                                                                                                           note= "cleavage generates mature protein"
                                                                                                                                                                                                                                                                                                                                                                              label= Potential proteolytic_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 629; DB 19; 100.0%; Pred. No. 3.3e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 126;
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RESULT 6
AAB73182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of the C-terminal region of the GDF-8 precursor protein. The predicted GDF-8 sequence contains two potential proteolytic processing sites.

Cleavage of the precursor at the second of these sites would generate a mature C terminal fragment 109 amino acids in length with a predicted molecular weight of 12,400.

GDF-8 has been shown to result in increased bone and muscle mass (such as ribs) when expressed in reduced amounts. GDF-8 minus transgenic animals and forms of animal feed that can inhibit/reduce production of GDF-8 are of commercial interest.
New substantially purified growth differentiation factor-8 polypeptide, useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome and cacheria
                                                                                                                                                                                                                                                                                                                                                                                                         Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia; neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculodegenerative disease; tissue repair; muscle wasting disease; neuromuscular disorder; spinal cord injury; traumatic injury; congestive obstructive pulmonary disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of muscle, bone or adipose tissue. A GDF-8 expression may also have a role in the therapy of abnormal growth of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8 antisense molecule or dominant negative polypeptide could be used with foetal or adult muscle cells, bone cells or progenitor cells. These agents can be administered to a patient suffering from a disorder such as muscle wasting disease, neuro muscular disorder, muscle atrophy, costeoporosis, bone degenerative diseases, obesity or other adipocyte
                                                                                                                                                                                                                                                                                                                                                                        Mus sp
                                                                                         N-PSDB; AAF63547.
                                                                                                                                                 Lee S,
                                                                                                                                                                                                                                                           17-AUG-2000; 2000WO-US22884.
                                                                                                                                                                                                                                                                                                                                      WO200112777-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine GDF-8 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB73182 standard; Protein; 126 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 2a; 138pp; English.
                                                                                                                                                                                   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                            2001-211209/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders, and aging for example.
                                                                                                                                                 McPherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                          99US-0378238.
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Pred. No. 3.3e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia; neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculodegenerative disease; tissue repair; muscle wasting disease; neuromuscular disorder; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           muscular dystrophy), musculodegenerative diseases or in tissue repair due to trauma, obesity and disorders related to abnormal proliferation of adipocytes. ODF-8 is also useful for treating malignancies of the various organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, spinal cord injury, traumatic injury, congestive obstructive pulmonary disease
                                                                               New substantially purified growth differentiation factor-8 polypeptide, useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromouscular disorder, acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to growth differentiation factor-8 (GDF-8) coding sequences and proteins. The present sequence is a GDF-8 protein, which was isolated in the present invention. GDF-8 is useful for treating neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular diseases (e.g. amyotrophic).
                                                                                                                                                         N-PSDB; AAF63555.
                                                                                                                                                                                                            Lee S, McPherron AC;
                                                                                                                                                                                                                                                                                  19-AUG-1999;
                                                                                                                                                                                                                                                                                                                    17-AUG-2000; 2000WO-US22884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                             Example 9; Fig 2; 124pp; English.
                                                                                                                                                                         WPI; 2001-211209/21.
                                                                                                                                                                                                                                                                                                                                                        22-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                          WO200112777-A2
                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                             traumatic injury; congestive obstructive pulmonary disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COPD), AIDS or cachexia.
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                                                                                                                                                                                                                                                (UYJO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VHQANDRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VHQANDRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                              UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                  99US-0378238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 629; DB 22;
Pred. No. 3.3e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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The present invention relates to growth differentiation factor-8 (GDF-8)

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RESULT 8
AAB20153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiant; human; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin; T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Growth differentiation factor 8 AutoVac construct GDF-8 ext.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB20153;
(MEBI-) M & E BIOTECH AS
                                                  20-JUL-1999;
26-JUL-1999;
                                                                                                                          20-JUL-2000; 2000WO-DK00413.
                                                                                                                                                                                     25-JAN-2001.
                                                                                                                                                                                                                                          WO200105820-A2.
                                                                                                                                                                                                                                                                                                                         Misc-difference 141..142
                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB20153 standard; Protein; 160 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COPD), AIDS or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPGLDCDEHSTESRCCRYPLTVDFBAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
Clostridium tetani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 629; DB 22; ilarity 100.0%; Pred. No. 3.4e-60; Conservative 0; Mismatches 0;
                                                  99DK-0001014
99US-0145275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16..36
                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                           /note= "Cys-124 may be substituted by Ser to avoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52..160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "identical to residues 215-230 of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "tetanus toxoid P30 epitope"
                                                                                                                                                                                                                                                                                            "optionally replaced by Glu-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                             "identical to residues 267-375 of human GDF-8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "tetanus toxoid P2 epitope"
                                                                                                                                                                                                                                                                                                                                                  disulfide bond formation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of AutoVac construct GDF-8 ext, which consists of the C-terminal 160 amino acids of human growth differentiation factor 8 (GDF-8, see AAF20131) with residues 16-36 cc differentiation factor 8 (GDF-8, see AAF20131) with residues 16-36 cc substituted by the promiscuous tetanus toxin T-cell epitope P30 (see AAF20144) and residues 37-51 substituted by tetanus toxin T-cell epitope P2 (see AAF20143). It is an object of the invention to produce a recombinant therapeutic vaccine that is capable of effecting comparison of GDF-8 in order to increase the muscle growth rate of farm animals. The vaccines (see AAF20145-53) are capable of breaking autotolerance against autologous GDF-8. They comprise the C-terminal portion of human GDF-8 in which a portion of the native sequence is replaced by a T-cell epitope such as P30, with minimal disturbance of the authentic 3-dimensional structure of the protein. Mucleic acids encoding the GDF-8 variants can be used to repetic immunisation of the animals. Down-regulation of GDF-8 cctivity can increase muscle mass by up to at least 45% in Cattle, pigs and poultry used for meat production, reducing the need for pigs and poultry used for meat production, reducing the need for antihiotic feed-additives. Anti-GDF8 vaccines can be used to treat human diseases such as cancer cachexia where muscle atrophy is pronounced and for patients suffering from acute and chronic heart continues the suffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                        Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia; neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculodegenerative disease; tissue repair; muscle wasting disease; neuromuscular disorder; spinal cord injury; traumatic injury; congestive obstructive pulmonary disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                               Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken GDF-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB73188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB73188 standard; Protein; 226 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 107-108; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   animal through induction of anti-GDF-8 antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Increasing the muscle mass of animals used in meat production by down regulating growth differentiation factor 8 (GDP-8) activity in the asimal through induction of anti-cRP-8 antibody production -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-112680/12.
                                                                                       17-AUG-2000; 2000WO-US22884.
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                                                                                                                                                                               22-FEB-2001
                                                                                                                                                                                                                                                            WO200112777-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 DEGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tecar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VHQANPRGSAGECCTETKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouritsen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 629; DB 22;
100.0%; Pred. No. 4.2e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klysner S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to growth differentiation factor-8 (GDF-8) cocking sequences and proteins. The present sequence is a GDF-8 protein, which was isolated in the present invention. GDF-8 is useful for treating neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular dystrophy), musculodegenerative diseases or in tissue repair due to trauma, obesity and disorders related to abnormal proliferation of adipocytes. GDF-8 is also useful for treating malignancies of the various organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, spinal cord injury, traumatic injury, congestive obstructive pulmonary disease (COPD), AIDS or cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New substantially purified growth differentiation factor-8 polypeptide, useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                  Chimeric -
                                                                                                                                                                                                                                                                                                                                                      Growth differentiation factor 8 AutoVac construct GDF-8 dimer.
                        Misc-difference
                                                                                            Region
                                                                                                                              Region
                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                    Chimeric - Clostridium tetani.
                                                                                                                                                                                                                                                                                                                    Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;
                                                                                                                                                                                                                                                                                                                                                                                          30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB20152 standard; Protein; 254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 9; Fig 2; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-211209/21.
DB; AAF63554.
                                                                                                                                                                                                                                                                                                    epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McPherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                    human; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; S ilarity 100.0%; P Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
90..91
/note= "optionally replaced by Glu-Gly"
                                                                                                                                                                                                                                                                                                    down-regulation; vaccine; muscle; meat; cachexia;
                                                                                            /note=
125..1
                                                                                                                                110..124
                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                /note= "109 C-terminal residues of human GDF-8"
                                          note= "109 C-terminal residues of human GDF-8"
                                                                          note=
                                                                                            . 145
                                                          .254
                                                                          "tetanus toxoid P30 epitope"
                                                                                                            "tetanus toxoid P2 epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 629; DB 22;
Pred. No. 6.2e-60;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of AutoVac construct GDF-8 dimer comprising 2 copies of the 109-amino acid (C-terminal region of human CC growth differentiation factor 8 (GDF-8, see AAF20141) covalently connected through the p2 and p30 T-cell epitopes (see AAB20143-44) CC connected through the p2 and p30 T-cell epitopes (see AAB20143-44) CC of tetanus toxin. It is an object of the invention to produce a recombinant therapeutic vaccine that is capable of effecting CC compression of GDF-8 in order to increase the muscle growth crate of farm animals. The vaccines (see AAB20145-53) are capable of breaking autotolerance against autologous GDF-8. They comprise the C-terminal portion of human GDF-8 in which a portion of the native sequence is replaced by a T-cell epitope such as P30, with minimal disturbance of the authentic 3-dimensional structure of the protein. Nucleic acids encoding the GDF-8 variants can be used for genetic immunisation of the animals. Down-regulation of GDF-8 criivity can increase muscle mass by up to at least 45% in cattle, pigs and poultry used for meat production, reducing the need for antibiotic feed-additives. Anti-GDF9 vaccines can be used to treat human diseases such as cancer cachaxia where muscle atrophy is pronounced and for patients suffering from acute and chronic heart
                                                                                                                                                                                                                                                                                                                                                                                                             Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
Turkey growth differentiation factor 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Increasing the muscle mass of animals used in meat production by down regulating growth differentiation factor 8 (GDF-8) activity in the animal through induction of anti-GDF-8 antibody production -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 235..236
                                            30-APR-2001
                                                                                                                                AAB20132 standard; Protein; 362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 105-106; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-112680/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halkier T, Mouritsen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-2000; 2000WO-DK00413.
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                                                                                                                                                                                                                                                                                                                         146 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 205
                                                                                                                                                                                                                                     206 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                   61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                       1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99DK-0001014
99US-0145275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "optionally replaced by Glu-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 629; DB 2
100.0%; Pred. No. 7e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klysner S;
                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0;

Growth differentiation factor 8; GDF-8; myostatin; down-regulation; vaccine; muscle; meat; cachexia; cardiant; turkey.

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RESULT 12
AAU75623
ID AAU75623
XX AAU75
AC AAU75
XX AU75
XX Chick
XX Gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                        문
                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of turkey growth differentiation factor 8 (GDF-8), also called myostatin. It is an object of the invention to produce a recombinant therapeutic vaccine capable of effecting down-regulation of GDF-8 in order to increase the muscle growth rate of farm animals. Variants of GDF-8 (see AAB20145-53) are provided that are capable of breaking autotolerance against autologous GDF-8. These comprise a C-terminal portion of human CGDF-8 in which a portion of the native sequence is replaced by a Cr-cell epitope such as the promiscuous tetanus toxin T-cell epitope Tr-cell epitope such as the promiscuous tetanus toxin T-cell epitope for genetic immunisation of the animals. Down-regulation of GDF-8 in catile, pigs and poultry used for meat production, reducing the need for antibiotic feed-additives. Anti-GDF8 vaccines can be used to treat human diseases such as cancer cachexia where muscle atrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 109
                                Chicken; promyostatin; immunomodulator; antidepressant; anorectic; neuroprotective; antidiabetic; growth differentiation factor receptor; myostatin receptor; GDF, muscle tissue; adipose tissue; cachexia; wasting disorder; anorexia; muscular dystrophy; neuromuscular disease; metabolic disorder; obesity; type II diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         animal through induction of anti-GDF-8 antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUL-2000; 2000WO-DK00413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200105820-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meleagris gallopavo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 76-78; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Increasing the muscle mass of animals used in meat production by regulating growth differentiation factor 8 (GDF-8) activity in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-112680/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halkier T,
                                                                                                                                             Chicken promyostatin.
                                                                                                                                                                                 21-MAY-2002
                                                                                                                                                                                                                                                      AAU75623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEBI-) M & E BIOTECH AS.
                                                                                                                                                                                                                                                                                                                                                                                                                        254
                                                                                                                                                                                                                                                                                                                                                314 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ы
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pronounced and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                        VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                        DEGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                      standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouritsen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 629; DB 2: ilarity 100.0%; Pred. No. 1e-59; Conservative 0; Mismatches
                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99DK-0001014
99US-0145275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for patients suffering from acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klysner
                                                                                                                                                                                                                                                        374
                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               down
                                                                                                                                                                                                                                                                                                                                                                                                                            313
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RESULT 13
AAR63160
ID AAR63
XX AAR63
AC AAR63
AC AAR63
XX CJOWE
XX Growt
XX Growt
XX Growt
XX Adipo
XX Homo
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor (GDF) receptor, specifically a myostatin receptor, or its functional peptide portion. Also described is a method of modulating an effect of myostatin on a cell by contacting the cell with an agent that affects myostatin signal transduction in the cell. The method and the receptor are useful for ameliorating the severity of a pathological condition characterised by an abnormal amount, development or metabolic activity of muscle or adipose tissue in a subject, particularly a wasting disorder (e.g. cachexia, anorexia, muscular dystrophy or neuromuscular disease) or a metabolic disorder (e.g. obesity or type II diabetes). The present sequence represents the amino acid sequence of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New growth differentiation factor (GDF) receptors and modulators, useful for ameliorating wasting disorders such as cachexia, muscu dystrophy or neuromuscular disease or a metabolic disorder such a
                                                                                                                                                                                                                                                                                            Growth differentiation factor-8; GDF-8; cell proliferation; adipocyte; obesity; transforming growth factor-beta.
                                                                                                                                                                                                                                                                                                                                                                                   Human growth differentiation factor-8 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promyostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Fig 1; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     obesity or type II diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUL-2000; 2000US-0626896.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200210214-A2
                                                             18-MAR-1994;
                                                                                                                     29-SEP-1994
                                                                                                                                                                                WO9421681-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR63160 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ьосат
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFGLDCDEHSTESRCCRYPLTVDFBAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McPherron AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK15396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relates to a substantially purified growth differentiation
                                                             94WO-US03019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 629; DB 23; Pred. No. 1.1e-59; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cachexia, muscular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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19-MAR-1993;

93US-0033923

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RESULT 14
AAW69888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 109
                                                                                                         23-MAY-1997;
05-FEB-1997;
28-APR-1997;
                                                                                                                                                                                                                                                                                                    Growth differentiation factor-8; GDF-8; chicken; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 199
Q-PSDB;
Transgenic animals with gene for growth differentiation disrupted - have increased muscle and reduced cholestero
                                WPI, 1998-437444/37.
N-PSDB; AAV45819.
                                                                 Lee S,
                                                                                                                                                     05-FEB-1998;
                                                                                                                                                                          06-AUG-1998
                                                                                                                                                                                               WO9833887-A1
                                                                                                                                                                                                                             Cleavage-site
Protein
                                                                                                                                                                                                                                                                        Gallus
                                                                                                                                                                                                                                                                                           therapy.
                                                                                                                                                                                                                                                                                                                                                Chicken growth
                                                                                                                                                                                                                                                                                                                                                                       07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                            AAW69888;
                                                                                                                                                                                                                                                                                                                                                                                                                AAW69888 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDF-8 can be used to maintain cells before transplantation; to improve efficiency of cell fusion and to treat obesity or diseases related to abnormal adipocyte proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 58; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New growth differentiation factor 8 - useful for treatmen diagnosis of cell proliferative disorders esp. of muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS
                                                                                      ( OLYU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  نسو
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHQANPRGSAGPCCTFTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1994-316943/39.
DB; Q76372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109;
                                                                                                                                                                                                                                                                      đs
                                                                                      VIND
                                                                McPherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                     JOHNS HOPKINS
                                                                                                         97US-0862445.
97US-0795071.
97US-0847910.
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                                                                                                                                                                                                                                                                                                                                                differentiation
                                                                                                                                                    98WO-US02479
                                                                                                                                                                                                                           Location/Qualifiers
263..266
267..375
                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                 Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHOOL MED
                                                                                     SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 629; DB 1
Pred. No. 1.1e-5
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  factor-8
                                                                                                                                                                                                                                                                                                                                                                                                                B
  cholesterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 375;
           factor-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
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ACC XXX ACC XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGP-8 expression is disrupted or interfered with. Also claimed care: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb from these animals; (2) method for increasing muscle mass in animals by administering an antibody (Ab) that binds to GDF-8; (3) cinhibiting the action of GDF-8 by treating foteal or adult muscle or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic acid encoding a GDF-8 protein truncated by loss of the C-terminal active fragment. The transgenic animals have increased muscle mass and for poultry reduced cholesterol contents. Method (3) is used to treat muscle wasting or neuromuscular diseases, muscular atrophy and aging, particularly muscular dystrophy, spinal cord or traumatic injuries, congestive or obstructive lung disease, ADDS and againg, method (4) is used to treat cancer of muscle, connective tissue and bone, or obesity. Also (not claimed) GDF-8 can be used to maintain myoblasts intended for transplanting or to improve efficiency of fusion. Ab can be used to detect and capantify GDF-8 (particularly in muscle, for diagnosis or monitoring), also for immunotherapy and in vivo imaging.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                        Growth differentiation factor-8; GDF-8; pig; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
                                                                                                                                                                                                                     Key
Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ractor-8 (GDF-8), a novel member of the transforming growth factor-beta superfamily that appears to relate to various cell proliferative disorders, especially those involving muscle nerva
                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                             Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                            therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                              WO9833887-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW69891 standard; Protein; 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuromuscular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also use of GDF-8 inhibitors for treating cancer, obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the amino acid sequence of chicken growth differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                  Location/Qualifiers
263..266
267..375
/label= Mat_protein
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100.0%; Pred. No. 1.1e-59;
tive 0; Mismatches 0;
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98WO-US02479.

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                                                                                                                                                                                                                                                                                                                                CC factor-8 (GDF-8), a novel member of the transforming growth differentiation CC factor-8 (GDF-8), a novel member of the transforming growth factor-CC beta superfamily that appears to relate to various cell contends of the transforming growth factor-CC superfamily that appears to relate to various cell contends of the transforming provides normal additional contends of the sequence was deduced from a cDNA clone (see AAV4592) isolated from a skeletal muscle CDNA library. The CC invention provides novel mammalian and avian GDF-8 proteins (see CC AAW6983)-92). A transgenic non-human animal is claimed in which CC gdF-8 expression is disrupted or interfered with. Also claimed CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb CC from these animals; (2) method for increasing muscle mass in CC animals by administering an antibody (Ab) that binds to GDF-8; (3) city of GDF-8 by treating foetal or adult muscle cc acid encoding a GDF-9 protein truncated by loss of the C-terminal CC acid encoding a GDF-9 protein truncated by loss of the C-terminal CC acid encoding a GDF-9 protein truncated by loss of the C-terminal CC acid encoding a GDF-9 protein truncated by loss of the C-terminal CC acid encoding a GDF-9 protein truncated by loss of the C-terminal CC acid encoding a GDF-9 protein truncated by loss of the C-terminal CC and for poultry reduced cholesterol contents. Method (3) is used to treat muscle wasting or neuromuscular diseases, muscular atrophy CC and aging, particularly muscular diseases, muscular atrophy CC and aging, particularly muscular diseases, muscular atrophy CC and experional bone, or obstructive lung disease, AIDS and cachexia. Method (4) is used to treat cancer of muscle, can be used to maintain myoblasts intended for transplanting or to improve efficiency of fusion. Ab can be used to detect and CC annotify GDF-8 (particularly in muscle, for diagnosis or monitoring), CC also for immunotherapy and in vivo imaging.
                                                                                                                                                                                                   Matches 109;
                                                                                                                                                                                                                       Query Match
Best Local (
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05-FEB-1997;
28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contents, also use of GDF-8 inhibitors for treating cancer, obesity, neuromuscular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-437444/37.
N-PSDB; AAV45822.
                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 9; Fig 14f; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
327 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
                                                                                             267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                         61 VHQANDRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                            DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                 375 AA;
                                                                                                                                                                                              100.0%; Score 629; DB 19; Length 37 Nilarity 100.0%; Pred, No. 1.1e-59; Conservative 0; Mismatches 0; Indels
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97US-0795071.
97US-0847910.
                                                                                                                                                                                                                                           Length 375;
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Search completed: January 31, 2003, 18:20:10 Job time: 33 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
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Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

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6: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to a score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution. is the number of results predicted by chance to have a ster than or equal to the score of the result being printed,

## SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	629	100.0	126	9	US-09-859-211-6	Sequence 6, Appli
2	629	100.0	130	9	US-09-859-211-33	Sequence 33, Appl
w	629	100.0	226	ø	US-09-859-211-35	Sequence 35, Appl
4.	629	100.0	374	ø	US-09-841-730-8	Sequence 8, Appli
σı	629	100.0	375	9	US-09-841-730-2	Sequence 2, Appli
0	629	100.0	375	9	US-09-841-730-14	Sequence 14, Appl
7	629	100.0	375	9	US-09-841-730-18	Sequence 18, Appl
œ	629	100.0	375	9	US-09-859-211-14	•
9	629	100.0	375	ø	US-09-859-211-23	Sequence 23, Appl
10	629	100.0	375	9	US-09-859-211-27	•
11	629	100.0	375	9	US-09-859-211-29	•
12	629	100.0	375	10	US-09-454-540-5	Sequence 5, Appl:
13	629	100.0	376	9	US-09-841-730-4	Sequence 4, Appli
14	629	100.0	376	9	US-09-841-730-6	Sequence 6, Appli
15	629	100.0	376	9	US-09-859-211-12	Sequence 12, Appl
16	629	100.0	376	9	US-09-859-211-25	Sequence 25, Appl
17	629	100.0	376	9	US-09-813-398-38	Sequence 38, Appl
18	629	100.0	376	10	US-09-859-894A-11	Sequence 11, Appl
19	624	99.2	375	5	US-09-859-894A-5	Sequence 5, Appli

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Д	44	43	42	41	40	39	38	37	36	35	34	<u>၂</u>	32	<b>3</b> 1	30	29	28	27	26	25	24	23	22	21	20
232.5	242	242	242	242	242	242	512.5	564	564	570	581	581	581	581	581	581	581	590	618	618	619	619	622	623	623
37.0	38.5	38.5	38.5	38.5	38.5	38.5	81.5	89.7	89.7	90.6	92.4	92.4	92.4	92.4	92.4	92.4	92.4	93.8	98.3	98.3	98.4	98.4	98.9	99.0	99.0
118	408	408	121	121	120	120	128	157	136	374	408	407	407	407	407	126	126	108	375	375	375	375	109	375	375
12	9	ø	9	9	12	10	10	φ	9	9	9	10	10	10	9	10	5	φ	9	9	9	9	10	9	9
US-10-115-406-9	US-09-813-398-22	US-09-813-398-20	US-09-880-708-24	US-09-859-211-46	US-10-115-406-20	US-09-813-459-20	US-09-205-658-317	US-09-841-730-27	US-09-841-730-29	US-09-841-730-20	US-09-813-398-33	US-09-859-894A-2	US-09-454-540-6	US-09-454-540-2	US-09-841-730-25	US-09-859-894A-4	US-09-454-540-4	US-09-859-211-8	US-09-859-211-21	US-09-841-730-12	US-09-859-211-31	US-09-841-730-16	US-09-754-826-2	US-09-859-211-19	US-09-841-730-10
Sequence 9, Appil	sequence zz, Appr				Œ	sequence 20, Appl	<u>ب</u>	Sequence 27, Appr	2, 2,		•		•		-	-	_	Sequence 8, Appli	Sequence 21, Appl	Sequence 12, Appl	1 L	Sequence 16, Appl	`	•	

## ALIGNMENTS

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                                                                                                                                                                                                                                                                  ; ORGANISM: Mus musculus US-09-859-211-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILLING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR FILLING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR APPLICATION NUMBER: 08/947,910
PRIOR FILLING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/95,071
PRIOR APPLICATION NUMBER: 08/955,596
PRIOR APPLICATION NUMBER: 08/525,596
                                                                                                                                                                                                                                                                                                                       ; SEQ ID NO 6
; LENGTH: 126
; TYPE: PRT
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                                                                                                                                                        Query Match 100.0%; Score 629; DB 9; Best Local Similarity 100.0%; Pred. No. 1.9e-59; Matches 109; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lee, Se-Jin
APPLICANT: McCherron, Alexandra C.
APPLICANT: McCherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US94/03019 PRIOR FILING DATE: 1994-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1993-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 08/033,923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1995-10-2
                                                  1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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; Sequence 33, Application US/09859211
; Patent No. US20020157125A1
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR PPLICATION NUMBER: 08/862,445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR PILING DATE: 1997-02-05
PRIOR #PLICATION NUMBER: 08/525,596
PRIOR #PLING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
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CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR PPLICATION NUMBER: 08/862,445
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR PPLICATION NUMBER: 08/847,910
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR APPLICATION NUMBER: 08/95,071
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR PILING DATE: 1995-10-26
PRIOR PILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR FILING DATE: 1994-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 35, Application US/09859211 Patent No. US20020157125A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
APPLICANT: McPherron, Differentiation factor-8
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-5-15
CURRENT FILING DATE: 2001-6-16
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Best Local :
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GENERAL INFORMATION:
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APPLICANT: McPherron, Alex
TITLE OF INVENTION: GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1993-03-19
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PRIOR APPLICATION NUMBER: 08/033,923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 07265/144001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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100.0%; Pred. No. 2e-59;
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RESULT 5
US-09-841-730-2
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PRIOR APPLICATION NUMBER: 09/626,896
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
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                                                                                                    Sequence 2, Application US/09841730 Patent No. US20020157126A1 GENERAL INFORMATION:
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LENGTH: 226
TYPE: PRT
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SEQ ID NO 8
LENGTH: 374
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Best Local Similarity
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APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version
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APPLICANT: McHerron, Alexandra C.
APPLICANT: MCTON: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: GROWISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
FILE REFERENCE: JHUI470-2
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PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                             326
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100.0%; Pred. No. 5.9e-59;
ative 0; Mismatches 0;
  THEREOF, AND METHODS OF USING
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SEQ ID NO 2

; LENGTH: 375

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-841-730-2
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US-09-841-730-14
; Sequence 14, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Porcine
US-09-841-730-14
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CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR PILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: F886SEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
FILE REFERENCE: JUH1470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/625,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR PILING DATE: 1997-08-01
NUMBER OF SEO ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local (
                                                                                                                                                                                                   Matches
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APPLICANT: McPherron, Alexandra C.
327 VHQANDRGSAGDCCTDTKMSDINMLYFNGKEQIIYGKIDAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                    267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
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                                                                                                                              1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                             100.0%; Score 629; DB 9; Length 375; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 375
; TYPE: PRI
; ORGANISM: Homo sapiens
US-09-859-211-14
                                                                                                                                                                                                                                               APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C,
APPLICANT: McPherron, Alexandra C,
APPLICANT: McPherron, Alexandra C,
APPLICANT: McPherron, IPPERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR APPLICATION NUMBER: 08/95,071
PRIOR APPLICATION NUMBER: 08/95,596
PRIOR APPLICATION NUMBER: 80/9525,596
PRIOR APPLICATION NUMBER: 807/US94/03019
PRIOR APPLICATION NUMBER: 807/US94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 08/953,596
PRIOR APPLICATION NUMBER: 807/US94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR FILING DATE: 1994-03-18
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CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR PRILING DATE: 198-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FRSETSEQ for Windows Version 4.0
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; Patent No. US20020157126A1
; GENERAL INFORMATION:
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Best Local (
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APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
FILE REFERENCE: JHU1470-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Meleagris gallopavo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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RESULT 10
US-09-859-211-27
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APPLICANT: McPherron, Alexandra C.
PITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-B
FILE REFERENCE: 07265/144001
CURRENT PAPLICATION UNMEER: 09/019/959,211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION UNMEER: 09/019,070
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION UNMEER: 08/862,445
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-05-23
PRIOR PEPLICATION UNMEER: 08/847,910
PRIOR FILING DATE: 1997-02-05
PRIOR FILING DATE: 1997-02-05
PRIOR FILING DATE: 1997-02-05
PRIOR FILING DATE: 1997-02-05
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PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SOFTWARE: RestSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 375
                                                                                                                                                                                                                             Sequence 27, Application US/09859211
Patent No. US20020157125A1
GENERAL INFORMATION:
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APPLICANT: Lee, Se-Jin
APPLICANT: McCherron, Alexandra C.
APPLICANT: McCherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENC' APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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ORGANISM: Gallus gallus
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FILLING DATE: 1997-02-05
FILLING DATE: 1995-10-26
APPLICATION NUMBER: PCT/US94/03019
FILLING DATE: 1994-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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100.0%; Pred. No. 5.9e-59;
Live 0; Mismatches 0; Indels (
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PRIOR REPLICATION NUMBER: 09/019,070

PRIOR APPLICATION NUMBER: 09/019,070

PRIOR APPLICATION NUMBER: 08/862,445

PRIOR APPLICATION NUMBER: 08/862,445

PRIOR PILING DATE: 1997-05-23

PRIOR PILING DATE: 1997-04-28

PRIOR PELICATION NUMBER: 08/95,071

PRIOR PILING DATE: 1997-02-05

PRIOR PILING DATE: 1997-03-18

PRIOR PILING DATE: 1997-03-18

PRIOR PILING DATE: 1997-03-18

PRIOR PILING DATE: 1997-03-18

PRIOR APPLICATION NUMBER: 08/033,923

PRIOR PILING DATE: 1993-03-19

PRIOR PILING DATE: 1993-03-19
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PRIOR FILLING DATE: 1997-05-23
PRIOR PPLICATION NUMBER: 08/847,910
PRIOR FILLING DATE: 1997-04-28
PRIOR FILLING DATE: 1997-04-28
PRIOR FILLING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR PILLING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR APPLICATION NUMBER: 08/03,923
PRIOR FILLING DATE: 1994-03-18
PRIOR PILLING DATE: 1993-03-19
PRIOR FILLING DATE: 1993-03-19
PRIOR FILLING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                                                                                        SOFTWARE: Fas
SEQ ID NO 29
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                            Matches 109;
                                                                                                                                                                    Query Match
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Best Local :
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APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
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                                       1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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                                                                                                                                       100.0%; Score 629; DB 9; 100.0%; Pred. No. 5.9e-59;
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                                                                                                                Mismatches
                                                                                                                                                                 Length 375;
                                                                                                                Indels
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Sequence 4, Application US/09841730 Patent No. US20020157126A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09454540 Patent No. US20010053358A1 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IPM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/454,540
FILING DATE: 06-DEC-1999
CLASSIFICATION:
CLASSIFICATION:
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CITY: La Jolla
CTATE: California
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TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HALLE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: (
FILING DATE: Februar)
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PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 376
                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 6
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CURRENT APPLICATION NUMBER: US/09/841,730

CURRENT FILING DATE: 2001-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: JHU1470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
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PRIOR TILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWIH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1997-08-01
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APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                 LENGTH: 37
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                             ORGANISM: Rattus norvegicus
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                                                268 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 327
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  61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                 Local Similarity
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100.0%; Pred. No. 5.9e-59;
tive 0; Mismatches 0;
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Pred. No. 5.9e-59;
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RESULT 15

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US-09-859-211-12
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IS EQUARDED TO US A POPUL CARLO US A POPUL CANTIL OR US A PRIOR FILING DATE: 1997-03-23
PRIOR FILING DATE: 1997-04-28
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Database :
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/pcodata/1.

2: /cgn2_6/pcodata/1.

3: /cgn2_6/pcodata/1.

4: /cgn2_6/pcodata/1.

5: /cgn2_6/pcodata/1.

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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
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US-09-451-501-14
US-09-451-501-12
US-09-451-501-21
US-09-451-501-23
US-09-451-501-27
US-08-525-5968-12
US-09-17-860A-12
US-08-891-7898-6
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US-08-75-5-671-5

US-08-795-671-5

US-09-177-860A-14

US-09-252-149B-29

US-09-252-149B-34

US-09-252-149B-34

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US-09-177-860A-6
US-09-378-238-6
US-09-451-501-6
US-09-378-238-21
US-09-378-238-19
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Sequence 6, Appli
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                                                        Query Match
Best Local Similarity
Matches 109; Conserv
      1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGBCEFVFLQKYPHTHL 60
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Regult No.

	100.0 376 4 US-09-451-301-30 Sequence 98.4 375 4 US-09-252-149B-30 Sequence 98.3 375 3 US-08-891-789B-2 Sequence 98.3 375 4 US-09-252-149B-31 Sequence 98.3 375 4 US-09-378-238-8 Sequence 98.4 108 2 US-09-378-238-8 Sequence 92.4 126 1 US-08-452-772-2 Sequence 92.4 126 2 US-08-452-772-2 Sequence 92.4 126 4 US-09-378-238-2 Sequence 92.4 126 4 US-09-414-234-2 92.4 126 5 US-08-247-907A-11 Sequence 92.4 362 1 US-08-247-907A-11 Sequence	45	44	43	42	41	40	39	38	37	36	35	34	ω G	32	31	30	29	28
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4 US-09-252- 4 US-09-252- 3 US-08-891- 4 US-09-252- 4 US-09-252- 4 US-09-252- 2 US-09-177- 3 US-09-278- 4 US-09-378- 4 US-09-451- 1 US-08-765- 2 US-08-765- 3 US-08-765- 3 US-08-795- 4 US-08-919- 5 PCT-US94-0	4 US-09-252-149B-30 Sequence 4 US-09-252-149B-30 Sequence 3 US-08-891-789B-2 Sequence 4 US-09-252-149B-31 Sequence 4 US-09-252-149B-32 Sequence 4 US-09-252-149B-31 Sequence 5 US-09-252-149B-31 Sequence 6 US-09-252-149B-31 Sequence 7 US-09-378-238-8 Sequence 7 US-09-378-238-8 Sequence 8 US-09-378-238-8 Sequence 9 US-09-451-501-8 Sequence 1 US-08-452-772-2 Sequence 1 US-08-75-4 Sequence 1 US-08-75-875-4 Sequence 1 US-08-919-850-2 Sequence 5 PCT-US94-0528B-2 Sequence 5 PCT-US94-0528B-2 Sequence 1 US-08-247-907A-11 Sequence	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	93.8	93.8	93.8	93.8	98.3	98.3	98.3	98.4		٠
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	-09-252-149B-30 Sequence -09-252-149B-30 Sequence -09-252-149B-3 Sequence -09-252-149B-2 Sequence -09-252-149B-3 Sequence -09-252-149B-3 Sequence -09-252-149B-3 Sequence -09-252-149B-3 Sequence -09-378-238-8 Sequence -09-378-238-8 Sequence -09-378-238-8 Sequence -09-378-238-8 Sequence -09-415-501-8 Sequence -08-452-772-2 Sequence -08-452-772-2 Sequence -08-452-875-4 Sequence -08-452-875-4 Sequence -08-95-671-4 Sequence -08-95-671-4 Sequence -08-919-850-2 Sequence -08-919-850-2 Sequence -08-247-907A-11 Sequence	ب	თ	4	4	ω	N	m	ب	4	4	ω	N	4,	4	w	4.	4	4
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ALIGNMENTS

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FILING DATE: 19-SEP-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
APPLICATION NUMBER: PCT/US94/07762
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., ph.D, John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07265/075001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 TELEPAX: 619-6/8-00/6: INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: FRIGHT: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,596B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                           MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 4225 EX
CITY: La Jolla
STATE: CA
                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                               amino acid
100.0%; Score 629; DB 2; ilarity 100.0%; Pred. No. 3.7e-66; Conservative 0; Mismatches 0;
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APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
               APPLICANT: Lee, Se-Jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 6:
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: Windows95
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/525,596
FILING DATE: 19-5EP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D, Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 858-677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                 78
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REFERENCE/DOCKET NUMBER: 07265/075003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                               INFORMATION:
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5. 6096506
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)GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 629; DB 3; Length 126; ilarity 100.0%; Pred. No. 3.7e-66; Conservative 0; Mismatches 0; Indels
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SYSTEM: Windows95
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FILE REFERENCE: JHU1120-9
CURRENT APPLICATION NUMBER: US/09/378,238
CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER FILING DATE: 1995-10-25
EARLIER FILING DATE: 1993-03-19
EARLIER APPLICATION NUMBER: PCTUS94/03019
EARLIER APPLICATION NUMBER: 08/033,923
EARLIER APPLICATION NUMBER: 08/033,923
EARLIER FILING DATE: 1993-03-19
PUMBER OF SEQ ID NOS: 41
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US-09-451-501-6
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GENERAL INFORMATION:
GENERAL INFORMATION: GROWTH DIFFERENTIATION FACTOR-8
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
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ORGANISM: Mus musculus
                                                                        INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                        APPLICATION NUMBER: 08/795,071
FILING DATE: «Unknowns
APPLICATION NUMBER: PCT/US94/03019
APPLICATION NUMBER: PCT/US94/03019
FILING DATE: 18-MASCh-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/105001
TELECOMMUNICATION NEORMATION:
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APPLICATION NUMBER: US/09/451,501
FILING DATE: 30-NO. 6468535-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                            SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
       TYPE: amino acid
                                                                                               TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
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APPLICANT: LOC, Se-Jin
APPLICANT: McPherron, Alexandra C.
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
FILE REFERENCE: JHU1120-9
CURRENT APPLICATION NUMBER: US/09/378,238
CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1997-02-05
EARLIER FILING DATE: 1995-10-25
EARLIER APPLICATION NUMBER: PCT/US94/03019
EARLIER APPLICATION NUMBER: DS/033,923
EARLIER APPLICATION NUMBER: 08/033,923
EARLIER FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 41
COMMENDER SECTION OF SECTION 
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GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Lee, Se-Jin
APPLICANT: McPheerron, Alexandra C.
APPLICANT: MCPHEERRON; GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
FILE REFERENCE: JHU1120-9
FULE REFERENCE: JHU1120-9
CURRENT APPLICATION NUMBER: US/09/378,238
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Best Local Similarity
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Best Local Similarity
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TYPE: PR
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No. 6465239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09378238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 629; DB 4; ilarity 100.0%; Pred. No. 3.8e-66; Conservative 0; Mismatches 0;
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Best Local Similarity luu...
109; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08525596B Patent No. 5827733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER FILING DATE: 1997-02-05
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER APPLICATION NUMBER: PCT/US94/03019
EARLIER FILING DATE: 1995-10-18
EARLIER FILING DATE: 1994-03-18
EARLIER APPLICATION NUMBER: 08/033,923
                                                                                                                                                                       APPLICATION NUMBER: PCT/US94/I
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D, J.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
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TYPE: PRT
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                                                                                                                     TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                      PAIDLE STATION: 514
PRIOR APPLICATION DATA:
PCT/US94/07762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 19-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
                                         TOPOLOGY:
                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400
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                                         linear
                                                                                                                                                              619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette
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                                                                                                                                                                                                                                            Ph.D, John R.
                                                                                                                         14:
                                                                                                                                                                                                     07265/075001
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US-08-525-596B-14

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US-08-765-875-5
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Patent No. 591423
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Best Local
                                                                               Matches 109;
                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFFLACATION NUMBER: US/08/272,763
ETILING DATE: 08-ULL-1994
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN PH.D., LISA A.
REGISTRATION NUMBER: P-38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                  MOLECULE TYPE: protein IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT AppliCATION DATA:
APPLICATION NUMBER: US/08/765,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SERSIEEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LEE, SB-JIN
APPLICANT: MCPHERRON, ALEXANDRA C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                 FEATURE:
267 DFGLDCDEHSTESRCCRYPLTVDFBAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
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                                                                                                                                                                         NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                    CLONE:
                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                           1, DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
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                                                                               Conservative
                                                                                                                                                                           Protein
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                                                                       100.0%; Score 629; DB 2;
100.0%; Pred. No. 1.3e-65;
. Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/272,763
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                                                                                                                   Length 375;
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FEATURE:
NAME/KEY:
LOCATION:
US-08-795-671-5
                Sequence 14, Application US/09177860A
PATENT NO. 6096506
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN INVESTOR OF SEQUENCES: 32
                                                                                                                                                                 RESULT 10
US-09-177-860A-14
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,671
FILING DATE: February 6, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: HALLE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 39.7265/106001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Se-Jin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFFILICANT: Se-Jin Lee and Alexandra McPherron TITLE OF INVENTION: GROWTH DIFFFURNTATIONS OF A PROPERTY OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: pro
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 326
                                                                                                                                                                                                                                                      327 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 375 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 629; DB 3;
100.0%; Pred. No. 1.3e-65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 375;
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ADDRESSEE:

E: Gray Cary Ware & Freidenrich LLP 4365 Executive Drive, Suite 1600

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US-09-177-860A-14
                                                                                             US-09-252-149B-29
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                                                                                                                                                                                                                        Sequence 29, Application US/09252149B
Patent No. 6369201
GENERAL INFORMATION:
APPLICANT: Barker, Christopher A.
APPLICANT: Morsey, Mohamad
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
TITLE OF INVENTION: VERTEBRATE SUBJECTS
FILE REFERENCE: 9001-0042
CURRENT APPLICATION UNMEER: US/09/252,149B
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION UNMEER: 60/075,213
PRIOR APPLICATION UNMEER: 00/075,213
PRIOR APPLICATION UNMEER: 030-19
NUMBER OF SEQ ID NOS: 39
NUMBER OF SEQ ID NOS: 39
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 375
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Best Local S
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Matches 109; Conservative
                                              Query Match
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ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D. Liss A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858 677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 858-677-1456
TELEPAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 375 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: "J. CITY: San Diego
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                           Local
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100.0%; Score 629; DB 4; Length 375; Similarity 100.0%; Pred No. 1 3e-65; 10618 09; Conservative 0; Mismacches 0; Indels
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for Windows Version 2.0
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Sequence 32. Application US/09252149B

Sequence 32. Application US/09252149B

Patent No. 6369201

GENERAL INFORMATION:

APPLICANT: Morsey, Mohamad

TITLE OF INVENTION: VERTEBRATE SUBJECTS

FILE REFERENCE: 9001-0042

CURRENT APPLICATION UNMBER: US/09/252,149B

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: 60/075,213

PRIOR APPLICATION NUMBER: 60/075,213

PRIOR REPLING DATE: 1998-02-19

NUMBER OF SEQ ID NOS: 39

SEQ ID NO 32

TYDE: DETERMENT DATE: 1998-02-19

LENGTH; 375
                                                                                                                                                                                  GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Barker, Christopher A.
APPLICANT: Barker, Christopher A.
APPLICANT: Barker, Christopher A.
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
TITLE OF INVENTION: VERTEBRATE SUBJECTS
FILE REFERENCE: 9001-0042
CURRENT APPLICATION NUMBER: US/09/252,149B
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: 60/075,213
FRIOR FILING DATE: 1998-02-19
INUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 375
TYPE: PRT
ORGANISM: Gallus gallus
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US-09-252-149B-34
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                                                                                                                 Query Match
Best Local &
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Best Local :
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ORGANISM: Sus scrofa
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                               1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                     tch 100.0%; Score 629; DB 4; Length 375; al Similarity 100.0%; Pred. No. 1.3e-65; 109; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 100.0%; Score 629; DB 4; Length 375; Similarity 100.0%; Pred. No. 1.3e-65; 09; Conservative 0; Mismatches 0; Indels (
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61 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109

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PATENT PILING DATE: 1995-10-25

FARLICER PILING DATE: 08/525,596

FARLICER PILING DATE: 1995-03-18

FARLICER PILING DATE: 1995-03-18

FARLICER PILING DATE: 1995-03-18

FARLICER PILING DATE: 1995-03-18

FARLIER PILING DATE: 1993-03-19

FARLIER PILING DATE: 1993-03-19
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; Sequence 35, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: VERTEBRATE SUBJECTS
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION UNMEER: US/09/252,149B
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/075,213
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 35
; LENGTH: 375
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                                                                                                                                                               ; TYPE: PRT; ORGANISM: Homo sapiens US-09-378-238-14
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100.0%; Score 629; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels
Ouery March

100.0%; Score 629; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels
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Search completed: January 31, 2003, 18:18:23 Job time : 12.5 secs